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(71) Applicant (*for all designated States except US*): **UNIVERSITY OF DELAWARE** [US/US]; 210 Hullihen Hall, Newark, DE 19716 (US).

(72) Inventors; and
(75) Inventors/Applicants (*for US only*): **KMIEC, Eric, B.** [US/US]; 18 Crossan Court, Landenberg, PA 19350 (US). **GAMPER, Howard, B.** [US/US]; 904 Locust Street, Philadelphia, PA 19107 (US). **RICE, Michael, C.** [US/US]; 802 Washington Crossing Road, Newtown, PA 18940 (US). **KIM, Jungsup** [KR/US]; 3 Chase Hall, Newark, DE 19711 (US).

(74) Agents: **HALEY, James, F., Jr.** et al.; Fish & Neave, 1251 Avenue of the Americas, New York, NY 10020 (US).

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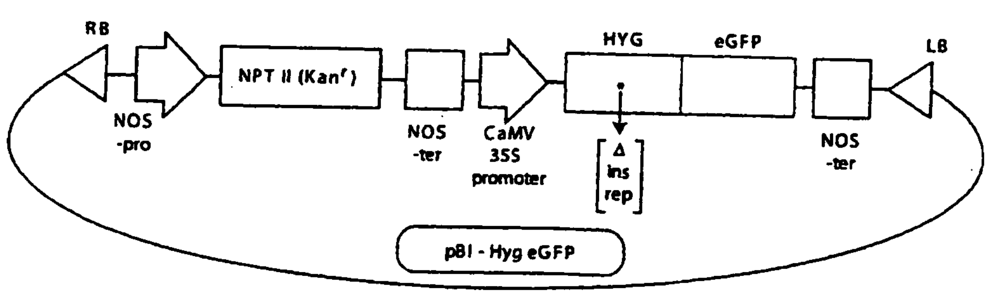
[Continued on next page]

(54) Title: TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES



(57) Abstract: Presented are methods and compositions for targeted chromosomal genomic alterations with modified single-stranded oligonucleotides. The oligonucleotides of the invention have modified nuclease-resisant termini comprising LNA, phosphorothioate linkages or 2'-O-Me base analogues or combinations of such modifications.

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TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

Field Of The Invention

The technical field of the invention is oligonucleotide-directed repair or alteration of plant genetic information using novel chemically modified oligonucleotides.

Background Of The Invention

A number of methods have been developed specifically to alter the genomic information of plants. These methods generally include the use of vectors such as, *for example*, T-DNA, *carrying* nucleic acid sequences encoding partial or complete portions of a particular protein which is expressed in a cell or tissue to effect the alteration. The expression of the particular protein then results in the desired phenotype. See, for example, United States Patent 4,459,355 which describes a method for transforming plants with a DNA vector and United States Patent 5,188,642 which describes cloning or expression vectors containing a transgenic DNA sequence which when expressed in plants confers resistance to the herbicide glyphosate. The use of such transgene-containing vectors adds one or more exogenous copies of a gene in a usually random fashion at one or more integration sites of the plant's genome at some variable frequency. The introduced gene may be foreign or may be derived from the host plant. Any gene which was originally present in the genome, which may be, for example, a normal allelic variant, mutated, defective, and/or functional copy of the introduced gene, is retained in the genome of the host plant.

These methods of gene alteration are problematic in that complications which can compromise the vigor, productivity, yield, etc. of the plant may result. One such problem is that insertion of exogenous nucleic acid at random location(s) in the genome can have deleterious effects. The random nature of this insertion and/or the use of exogenous promoters can also cause the timing, location or strength of expression of the introduced transgene to be inappropriate or unpredictable. Another problem with such systems includes the addition of unnecessary and unwanted genetic material to the genome of the recipient, including, for example, T-DNA ends or other vector remnants, exogenous control sequences required to allow production of the transgene protein, which control sequences may be

exogenous or native to the host plant and/or the transgene, and reporter genes or resistance markers. Such remnants and added sequences may have presently unrecognized consequences, for example, involving genetic rearrangements of the recipient genomes. In addition, concerns have been raised with consumption, especially by humans, of plants containing such exogenous genetic material.

More recently, simpler systems involving poly- or oligo- nucleotides have been described for use in the alteration of genomic DNA. These chimeric RNA-DNA oligonucleotides, requiring contiguous RNA and DNA bases in a double-stranded molecule folded by complementarity into a double hairpin conformation, have been shown to effect single basepair or frameshift alterations, for example, for mutation or repair of plant, animal or fungal genomes. See, for example, WO 99/07865 and U.S. Patent 5,565,350. In the chimeric RNA-DNA oligonucleotide, an uninterrupted stretch of DNA bases within the molecule is required for sequence alteration of the targeted genome while the obligate RNA residues are involved in complex stability. Due to the length, backbone composition, and structural configuration of these chimeric RNA-DNA molecules, they are expensive to synthesize and difficult to purify. Moreover, if the RNA-containing strand of the chimeric RNA-DNA oligonucleotide is designed so as to direct gene alteration, a series of mutagenic reactions resulting in nonspecific base alteration can result. Such a result reduces the utility of such a molecule in methods designed for targeted gene alteration.

Alternatively, other oligo- or poly- nucleotides have been used which require a triplex forming, usually polypurine or polypyrimidine, structural domain which binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide. Such oligonucleotides may have an additional DNA reactive moiety, such as psoralen, covalently linked to the oligonucleotide. These reactive moieties function as effective intercalation agents, stabilize the formation of a triplex and can be mutagenic. Such agents may be required in order to stabilize the triplex forming domain of the oligonucleotide with the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Patent 5,422,251. The utility of these oligonucleotides for directing targeted gene alteration is compromised by a high frequency of nonspecific base changes.

In more recent work, the domain for altering a genome is linked or tethered to the triplex forming domain of the bi-functional oligonucleotide, adding an additional linking or tethering functional domain to the oligonucleotide. See, e.g., Culver et al., Nature Biotechnology 17: 989-93 (1999). Such chimeric or triplex forming molecules have distinct structural requirements for each of the different domains of the complete poly- or oligo-nucleotide in order to effect the desired genomic alteration in either episomal or chromosomal targets.

Other genes, e.g. CFTR, have been targeted by homologous recombination using duplex fragments having several hundred basepairs. See, e.g., Kunzelmann et al., Gene Ther. 3:859-867 (1996). Similar efforts to target genes by homologous recombination in plants using large fragments of DNA had some success. See Kempin et al., Nature 389:802-803 (1997). However, the efficiency and reproducibility of the published homologous recombination approach in plants has severely limited the widespread use of this method.

Earlier experiments to mutagenize an antibiotic resistance indicator gene by homologous recombination used an unmodified DNA oligonucleotide rather than larger fragments of DNA, wherein the oligonucleotide had no functional domains other than a region of complementary sequence to the target. See Campbell et al., New Biologist 1: 223-227 (1989). These experiments required large concentrations of the oligonucleotide, exhibited a very low frequency of episomal modification of a targeted exogenous plasmid gene not normally found in the cell and have not been reproduced. However, as shown in examples herein, we have observed that an unmodified DNA oligonucleotide can convert a base at low frequency which is detectable using the assay systems described herein.

Oligonucleotides designed for use in the targeted alteration of genetic information are significantly different from oligonucleotides designed for antisense approaches. For example, antisense oligonucleotides are perfectly complementary to and bind an mRNA strand in order to modify expression of a targeted mRNA and are used at high concentration. As a consequence, they are unable to produce a gene conversion event by either mutagenesis or repair of a defect in the chromosomal DNA of a host genome. Furthermore, the backbone chemical composition used in most oligonucleotides designed for use in antisense approaches renders them inactive as substrates for homologous pairing or mismatch repair enzymes and the high concentrations of oligonucleotide required for antisense applications can be toxic with some types of nucleotide modifications. In addition, antisense oligonucleotides must be complementary to the mRNA and therefore, may not be complementary to the other DNA strand or to genomic sequences that span the junction between intron sequence and exon sequence.

Artificial chromosomes can be useful for the screening purposes identified herein. These molecules are man-made linear or circular DNA molecules constructed from essential cis-acting DNA sequence elements that are responsible for the proper replication and partitioning of natural chromosomes (Murray et al., 1983). The essential elements are: (1) Autonomous Replication Sequences (ARS), (2) Centromeres, and (3) Telomeres.

Yeast artificial chromosomes (YACs) allow large segments of genomic DNA to be cloned and modified (Burke et al., Science 236:806; Peterson et al., Trends Genet. 13:61 (1997); Choi, et al., Nat.

Genet., 4:117-223 (1993), Davies, et al., Biotechnology 11:911-914 (1993), Matsuura, et al., Hum. Mol. Genet., 5:451-459 (1996), Peterson et al., Proc. Natl. Acad. Sci., 93:6605-6609 (1996); and Schedl, et al., Cell, 86:71-82 (1996)). Other vectors also have been developed for the cloning of large segments of genomic DNA, including cosmids, and bacteriophage P1 (Sternberg et al., Proc. Natl. Acad. Sci. U.S.A., 87:103-107 (1990)). YACs have certain advantages over these alternative large capacity cloning vectors (Burke et al., Science, 236:806-812 (1987)). The maximum insert size is 35-30 kb for cosmids, and 100 kb for bacteriophage P1, both of which are much smaller than the maximal insert size for a YAC.

An alternative to YACs are cloning systems based on the *E. coli* fertility factor that have been developed to construct large genomic DNA insert libraries. They are bacterial artificial chromosomes (BACs) and P-1 derived artificial chromosomes (PACs) (Mejia et al., Genome Res. 7:179-186 (1997); Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Ioannou et al., Nat. Genet., 6:84-89 (1994); Hosoda et al., Nucleic Acids Res. 18:3863 (1990)). BACs are based on the *E. coli* fertility plasmid (F factor); and PACs are based on the bacteriophage P1. These vectors propagate at a very low copy number (1-2 per cell) enabling genomic inserts up to 300 kb in size to be stably maintained in recombination deficient hosts. The PACs and BACs are circular DNA molecules that are readily isolated from the host genomic background by classical alkaline lysis (Birnboim et al., Nucleic Acids Res. 7:1513-1523 (1979)). In addition, BACs have been developed for transformation of plants with high-molecular weight DNA using the T-DNA system (Hamilton, Gene 24:107-116 (1997); Frary & Hamilton, Transgenic Res. 10: 121-132 (2001)).

A need exists for simple, inexpensive oligonucleotides capable of producing targeted alteration of genetic material such as those described herein as well as methods to identify optimal oligonucleotides that accurately and efficiently alter target DNA.

Summary Of The Invention

Novel, modified single-stranded nucleic acid molecules that direct gene alteration in plants are identified and the efficiency of alteration is analyzed both *in vitro* using a cell-free extract assay and *in vivo* using a yeast system and a plant system. The alteration in an oligonucleotide of the invention may comprise an insertion, deletion, substitution, as well as any combination of these. Site specific alteration of DNA is not only useful for studying function of proteins *in vivo*, but it is also useful for creating plants with desired phenotypes, including, for example, environmental stress tolerance, improved nutritional value, herbicide resistance, disease resistance, modified oil production, modified starch production, and altered floral morphology including selective sterility. As described herein,

oligonucleotides of the invention target directed specific gene alterations in genomic double-stranded DNA in cells. The target genomic DNA can be nuclear chromosomal DNA as well as plastid or mitochondrial chromosomal DNA. The target DNA can also be a transgene present in the plant cell, including; for example, a previously introduced T-DNA. For screening purposes, the target plant DNA can also be extrachromosomal DNA present in plant or non-plant cells in various forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), as well as episomal DNA, including episomal DNA from an exogenous source such as a plasmid or recombinant vector. Many of these artificial chromosome constructs containing plant DNA can be obtained from a variety of sources, including, e.g., the Arabidopsis Biological Resource Center (ABRC) at the Ohio State University, and the Rice Genome Research Program at the MAFF DNA bank in Ibaraki, Japan. The target DNA may be transcriptionally silent or active. In a preferred embodiment, the target DNA to be altered is the non-transcribed strand of a genomic DNA duplex. In a more preferred embodiment, the target DNA to be altered is the non-transcribed strand of a transcribed gene of a genomic DNA duplex.

The low efficiency of targeted gene alteration obtained using unmodified DNA oligonucleotides is believed to be largely the result of degradation by nucleases present in the reaction mixture or the target cell. Although different modifications are known to have different effects on the nuclease resistance of oligonucleotides or stability of duplexes formed by such oligonucleotides (see, e.g., Koshkin et al., J. Am. Chem. Soc., 120:13252-3), we have found that it is not possible to predict which of any particular known modification would be most useful for any given alteration event, including for the construction of gene alteration oligonucleotides, because of the interaction of different as yet unidentified proteins during the gene alteration event. Herein, a variety of nucleic acid analogs have been developed that increase the nuclease resistance of oligonucleotides that contain them, including, e.g., nucleotides containing phosphorothioate linkages or 2'-O-methyl analogs. We recently discovered that single-stranded DNA oligonucleotides modified to contain 2'-O-methyl RNA nucleotides or phosphorothioate linkages can enable specific alteration of genetic information at a higher level than either unmodified single-stranded DNA or a chimeric RNA/DNA molecule. See, for example, copending applications United States application no. 60/208,538, United States application no. 60/244,989, United States application no. 09/818,875, international application no. PCT/US01/09761 and Gamper et al., Nucleic Acids Research 28: 4332-4339 (2000), the disclosures of which are incorporated herein in their entirety by reference. We also found that additional nucleic acid analogs which increase the nuclease resistance of oligonucleotides that contain them, including, e.g., "locked nucleic acids" or "LNAs", xylo-

LNAs and L-ribo-LNAs; see, for example, Wengel & Nielsen, WO 99/14226; Wengel, WO 00/56748; Wengel, WO 00/66604; and Jakobsen & Koshkin, WO 01/25478 also allow specific targeted alteration of genetic information.

The assay allows for determining the optimum length of the oligonucleotide, optimum sequence of the oligonucleotide, optimum position of the mismatched base or bases, optimum chemical modification or modifications, optimum strand targeted for identifying and selecting the most efficient oligonucleotide for a particular gene alteration event by comparing to a control oligonucleotide. Control oligonucleotides may include a chimeric RNA-DNA double hairpin oligonucleotide directing the same gene alteration event, an oligonucleotide that matches its target completely, an oligonucleotide in which all linkages are phosphorothiolated, an oligonucleotide fully substituted with 2'-O-methyl analogs or an RNA oligonucleotide. Such control oligonucleotides either fail to direct a targeted alteration or do so at a lower efficiency as compared to the oligonucleotides of the invention. The assay further allows for determining the optimum position of a gene alteration event within an oligonucleotide, optimum concentration of the selected oligonucleotide for maximum alteration efficiency by systematically testing a range of concentrations, as well as optimization of either the source of cell extract by testing different plants or strains, or testing cells derived from different plants or strains, or plant cell lines. Using a series of single-stranded oligonucleotides, comprising all RNA or DNA residues and various mixtures of the two, several new structures are identified as viable molecules in nucleotide conversion to direct or repair a genomic mutagenic event. When extracts from mammalian, plant and fungal cells are used and are analyzed using a genetic readout assay in bacteria, single-stranded oligonucleotides having one of several modifications are found to be more active than a control RNA-DNA double hairpin chimera structure when evaluated using an *in vitro* gene repair assay. Similar results are also observed *in vivo* using yeast, mammalian and plant cells. Molecules containing various lengths of modified bases were found to possess greater activity than unmodified single-stranded DNA molecules.

Detailed Description Of The Invention

The present invention provides oligonucleotides having chemically modified, nuclease resistant residues, preferably at or near the termini of the oligonucleotides, and methods for their identification and use in targeted alteration of plant genetic material, including gene mutation, targeted gene repair and gene knockout. The oligonucleotides are preferably used for mismatch repair or alteration by changing at least one nucleic acid base, or for frameshift repair or alteration by addition or deletion of at least one nucleic acid base. The oligonucleotides of the invention direct any such alteration,

including gene correction, gene repair or gene mutation and can be used, for example, to introduce a polymorphism or haplotype or to eliminate ("knockout") a particular protein activity. For example, gene alterations that knockout a particular protein activity can be obtained using oligonucleotides designed to convert a codon in the coding region of the protein to a stop codon, thus prematurely terminating translation of the protein. Oligonucleotides that introduce stop codons in the open-reading-frame of the protein are one embodiment of the invention. Generally, oligonucleotides that introduce stop codons early in the open-reading-frame of the protein are preferred. If the open-reading-frame contains more than one methionine, oligonucleotides that introduce stop codons after the second methionine are preferred. Additionally, if the gene exhibits alternative splice sites, oligonucleotides that introduce stop codons in exons after the alternative splice site are preferred. The following table provides examples of codons that can be converted to stop codons by altering a single oligonucleotide. A skilled artisan could readily identify other codons that can be converted to stop codons by altering one, two or three of the base pairs in a given codon. Similarly, a skilled artisan could readily identify codons that can be converted to stop codons by a frameshift mutations that inserts or deletes one or two base pairs in the open-reading-frame. It is also understood that more than one stop codon can be generated in a single open-reading-frame and that these stop codons can be adjacent in the sequence or separated by intervening codons. Where more than one stop codon is introduced into a single open-reading-frame, such alterations can be generated by a single or multiple oligonucleotides and can be generated simultaneously or by sequential mutagenesis of the target nucleic acid.

*Original codons**	*Corresponding stop codon*
GGA (glycine), **A**GA (arginine), **C**GA (arginine), T**T**A (leucine), T**C**A (serine), TG**T** (cysteine), TG**G** (tryptophan), TG**C** (cysteine)	TGA
AAG (lysine), **G**AG (glutamate), **C**AG (glutamine), T**T**G (leucine), T**C**G (serine), T**G**G (tryptophan), TA**T** (cysteine), TA**C** (tyrosine)	TAG
AAA (lysine), **G**AA (glutamate), **C**AA (glutamine), T**T**A (leucine), T**C**A (serine), TA**T** (cysteine), TA**C** (tyrosine)	TAA

*The amino acid encoded by the original codon is shown in parentheses and the base targeted for alteration to convert the codon to the corresponding stop codon is underlined and in bold

The oligonucleotides of the invention are designed as substrates for homologous pairing and repair enzymes and as such have a unique backbone composition that differs from chimeric RNA-DNA double hairpin oligonucleotides, antisense oligonucleotides, and/or other poly- or oligo-nucleotides used for altering genomic DNA, such as triplex forming oligonucleotides. The single-stranded oligonucleotides described herein are inexpensive to synthesize and easy to purify. In side-by-side comparisons, an optimized single-stranded oligonucleotide comprising modified residues as described herein is significantly more efficient than a chimeric RNA-DNA double hairpin oligonucleotide in directing a base substitution or frameshift mutation in a cell-free extract assay.

We have discovered that single-stranded oligonucleotides having a DNA domain surrounding the targeted base, with the domain preferably central to the poly- or oligo-nucleotide, and having at least one modified end, preferably at the 3' terminal region, are able to alter a target genetic sequence and with an efficiency that is higher than chimeric RNA-DNA double hairpin oligonucleotides disclosed in US Patent 5,565,350. Preferred oligonucleotides of the invention have at least two modified bases on at least one of the termini, preferably the 3' terminus of the oligonucleotide. Oligonucleotides of the invention can efficiently be used to introduce targeted alterations in a genetic sequence of DNA in the presence of human, animal, plant, fungal (including yeast) proteins and in cells of different types including, for example, plant cells, fungal cells including *S. cerevisiae*, *Ustillago maydis*, *Candida albicans*, and mammalian cells. Particularly preferred are cells and cell extracts derived from plants including, for example, experimental model plants such as *Chlamydomonas reinhardtii*, *Physcomitrella patens*, and *Arabidopsis thaliana* in addition to crop plants such as cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), fruits such as apples (*Malus*, e.g. *domesticus*), mangoes (*Mangifera*, e.g. *indica*), banana (*Musa*, e.g. *acuminata*), berries (such as currant, *Ribes*, e.g. *rubrum*), kiwifruit (*Actinidia*, e.g. *chinensis*), grapes (*Vitis*, e.g. *vinifera*), bell peppers (*Capsicum*, e.g. *annuum*), cherries (such as the sweet cherry, *Prunus*, e.g. *avium*), cucumber (*Cucumis*, e.g. *sativus*), melons (*Cucumis*, e.g. *melo*), nuts (such as walnut, *Juglans*, e.g. *regia*; peanut, *Arachis hypogeae*), orange (*Citrus*, e.g. *maxima*), peach (*Prunus*, e.g. *persica*), pear (*Pyra*, e.g. *communis*), plum (*Prunus*, e.g. *domestica*), strawberry (*Fragaria*, e.g. *moschata* or *vesca*), tomato (*Lycopersicon*, e.g. *esculentum*); leaves and forage, such as alfalfa (*Medicago*, e.g. *sativa* or *truncatula*), cabbage (e.g. *Brassica oleracea*), endive (*Cichoreum*, e.g. *endivia*), leek (*Allium*, e.g. *porrum*), lettuce (*Lactuca*, e.g. *sativa*), spinach (*Spinacia*, e.g. *oleraceae*), tobacco (*Nicotiana*, e.g. *tabacum*); roots, such as arrowroot (*Maranta*, e.g. *arundinacea*), beet (*Beta*, e.g. *vulgaris*), carrot (*Daucus*, e.g. *carota*), cassava (*Manihot*, e.g. *esculenta*), turnip (*Brassica*, e.g. *rapa*), radish (*Raphanus*, e.g. *sativus*), yam (*Dioscorea*, e.g. *esculenta*), sweet potato (*Ipomoea batatas*); seeds, including oilseeds,

such as beans (*Phaseolus*, e.g. *vulgaris*), pea (*Pisum*, e.g. *sativum*), soybean (*Glycine*, e.g. *max*), cowpea (*Vigna unguiculata*), mothbean (*Vigna aconitifolia*), wheat (*Triticum*, e.g. *aestivum*), sorghum (*Sorghum* e.g. *bicolor*), barley (*Hordeum*, e.g. *vulgare*), corn (*Zea*, e.g. *mays*), rice (*Oryza*, e.g. *sativa*), rapeseed (*Brassica napus*), millet (*Panicum* sp.), sunflower (*Helianthus annuus*), oats (*Avena sativa*), chickpea (*Cicer*, e.g. *arietinum*); tubers, such as kohlrabi (*Brassica*, e.g. *oleraceae*), potato (*Solanum*, e.g. *tuberosum*) and the like; fiber and wood plants, such as flax (*Linum* e.g. *usitatissimum*), cotton (*Gossypium* e.g. *hirsutum*), pine (*Pinus* sp.), oak (*Quercus* sp.), eucalyptus (*Eucalyptus* sp.), and the like and ornamental plants such as turfgrass (*Lolium*, e.g. *rigidum*), petunia (*Petunia*, e.g. x *hybrida*), hyacinth (*Hyacinthus orientalis*), carnation (*Dianthus* e.g. *caryophyllus*), delphinium (*Delphinium*, e.g. *ajacis*), Job's tears (*Coix lacryma-jobi*), snapdragon (*Antirrhinum majus*), poppy (*Papaver*, e.g. *nudicaule*), lilac (*Syringa*, e.g. *vulgaris*), hydrangea (*Hydrangea* e.g. *macrophylla*), roses (including Gallicas, Albas, Damasks, Damask Perpetuals, Centifolias, Chinas, Teas and Hybrid Teas) and ornamental goldenrods (e.g. *Solidago* spp.). Such plant cells can then be used to regenerate whole plants according to methods described herein or any method known in the art. The DNA domain of the oligonucleotides is preferably fully complementary to one strand of the gene target, except for the mismatch base or bases responsible for the gene alteration event(s). On either side of the preferably central DNA domain, the contiguous bases may be either RNA bases or, preferably, are primarily DNA bases. The central DNA domain is generally at least 8 nucleotides in length. The base(s) targeted for alteration in the most preferred embodiments are at least about 8, 9 or 10 bases from one end of the oligonucleotide.

According to certain embodiments, one or both of the termini of the oligonucleotides of the present invention comprise phosphorothioate modifications, LNA backbone (including LNA derivatives and analogs) modifications, or 2'-O-methyl base analogs, or any combination of these modifications. Oligonucleotides comprising 2'-O-methyl or LNA analogs are a mixed DNA/RNA polymer. The oligonucleotides of the invention are, however, single-stranded and are not designed to form a stable internal duplex structure within the oligonucleotide. The efficiency of gene alteration is surprisingly increased with oligonucleotides having internal complementary sequence comprising phosphorothioate modified bases as compared to 2'-O-methyl modifications. This result indicates that specific chemical interactions are involved between the converting oligonucleotide and the proteins involved in the conversion. The effect of other such chemical interactions to produce nuclease resistant termini using modifications other than LNA (including LNA derivatives or analogs), phosphorothioate linkages, or 2'-O-methyl analog incorporation into an oligonucleotide can not yet be predicted because the proteins

involved in the alteration process and their particular chemical interaction with the oligonucleotide substituents are not yet known and cannot be predicted.

In the examples, oligonucleotides of defined sequence are provided for alteration of genes in particular plants. Provided the teachings of the instant application, one of skill in the art could readily design oligonucleotides to introduce analogous alterations in homologous genes from any plant. Furthermore, in the tables of these examples, the oligonucleotides of the invention are not limited to the particular sequences disclosed. The oligonucleotides of the invention include extensions of the appropriate sequence of the longer 120 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Thus the oligonucleotides of the invention include for each correcting change, oligonucleotides of length 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. In some embodiments, longer nucleic acids of up to 240 bases which comprise the sequences disclosed herein may be used. Moreover, the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides of the invention as disclosed in the various tables for alteration of particular plant genes contain phosphorothioate linkages, 2'-O-methyl analog or LNA (including LNA derivatives and analogs) or any combination of these modifications just as the assay oligonucleotides do.

The present invention, however, is not limited to oligonucleotides that contain any particular nuclease resistant modification. Oligonucleotides of the invention may be altered with any combination of additional LNAs (including LNA derivatives and analogs), phosphorothioate linkages or 2'-O-methyl analogs to maximize conversion efficiency. For oligonucleotides of the invention that are longer than about 17 to about 25 bases in length, internal as well as terminal region segments of the backbone may be altered. Alternatively, simple fold-back structures at each end of a oligonucleotide or appended end groups may be used in addition to a modified backbone for conferring additional nuclease resistance.

The different oligonucleotides of the present invention preferably contain more than one of the aforementioned backbone modifications at each end. In some embodiments, the backbone modifications are adjacent to one another. However, the optimal number and placement of backbone modifications for any individual oligonucleotide will vary with the length of the oligonucleotide and the particular type of backbone modification(s) that are used. If constructs of identical sequence having

phosphorothioate linkages are compared, 2, 3, 4, 5, or 6 phosphorothioate linkages at each end are preferred. If constructs of identical sequence having 2'-O-methyl base analogs are compared, 1, 2, 3 or 4 analogs are preferred. The optimal number and type of backbone modifications for any particular oligonucleotide useful for altering target DNA may be determined empirically by comparing the alteration efficiency of the oligonucleotide comprising any combination of the modifications to a control molecule of comparable sequence using any of the assays described herein. The optimal position(s) for oligonucleotide modifications for a maximally efficient altering oligonucleotide can be determined by testing the various modifications as compared to control molecule of comparable sequence in one of the assays disclosed herein. In such assays, a control molecule includes, e.g., a completely 2'-O-methyl substituted molecule, a completely complementary oligonucleotide, or a chimeric RNA-DNA double hairpin.

Increasing the number of phosphorothioate linkages, LNAs or 2'-O-methyl bases beyond the preferred number generally decreases the gene repair activity of a 25 nucleotide long oligonucleotide. Based on analysis of the concentration of oligonucleotide present in the extract after different time periods of incubation, it is believed that the terminal modifications impart nuclease resistance to the oligonucleotide thereby allowing it to survive within the cellular environment. However, this may not be the only possible mechanism by which such modifications confer greater efficiency of conversion. For example, as disclosed herein, certain modifications to oligonucleotides confer a greater improvement to the efficiency of conversion than other modifications.

Efficiency of conversion is defined herein as the percentage of recovered substrate molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. the genome of a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be sequenced to determine the percentage that have acquired the desire change. The oligonucleotides of the invention in different embodiments can alter DNA two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold more than control oligonucleotides. Such control oligonucleotides are oligonucleotides with fully phosphorothiolated linkages, oligonucleotides that are fully substituted with 2'-O-methyl analogs, a perfectly matched oligonucleotide that is fully complementary to a target sequence or a chimeric DNA-RNA double hairpin oligonucleotide such as disclosed in US Patent 5,565,350.

In addition, for a given oligonucleotide length, additional modifications interfere with the ability of the oligonucleotide to act in concert with the cellular recombination or repair enzyme machinery

which is necessary and required to mediate a targeted substitution, addition or deletion event in DNA. For example, fully phosphorothiolated or fully 2-O-methylated molecules are inefficient in targeted gene alteration.

The oligonucleotides of the invention as optimized for the purpose of targeted alteration of genetic material, including gene knockout or repair, are different in structure from antisense oligonucleotides that may possess a similar mixed chemical composition backbone. The oligonucleotides of the invention differ from such antisense oligonucleotides in chemical composition, structure, sequence, and in their ability to alter genomic DNA. Significantly, antisense oligonucleotides fail to direct targeted gene alteration. The oligonucleotides of the invention may target either strand of DNA and can include any component of the genome including, for example, intron and exon sequences. The preferred embodiment of the invention is a modified oligonucleotide that binds to the non-transcribed strand of a genomic DNA duplex. In other words, the preferred oligonucleotides of the invention target the sense strand of the DNA, i.e. the oligonucleotides of the invention are complementary to the non-transcribed strand of the target duplex DNA. The sequence of the non-transcribed strand of a DNA duplex is found in the mRNA produced from that duplex, given that mRNA uses uracil-containing nucleotides in place of thymine-containing nucleotides.

Moreover, the initial observation that single-stranded oligonucleotides comprising these modifications and lacking any particular triplex forming domain have reproducibly enhanced gene alteration activity in a variety of assay systems as compared to a chimeric RNA-DNA double-stranded hairpin control or single-stranded oligonucleotides comprising other backbone modifications was surprising. The single-stranded molecules of the invention totally lack the complementary RNA binding structure that stabilizes a normal chimeric double-stranded hairpin of the type disclosed in U.S. Patent 5,565,350 yet is more effective in producing targeted base conversion as compared to such a chimeric RNA-DNA double-stranded hairpin. In addition, the molecules of the invention lack any particular triplex forming domain involved in Hoogsteen interactions with the DNA double helix and required by other known oligonucleotides in other oligonucleotide-dependant gene conversion systems. Although the lack of these functional domains was expected to decrease the efficiency of an alteration in a sequence, just the opposite occurs: the efficiency of sequence alteration using the modified oligonucleotides of the invention is higher than the efficiency of sequence alteration using a chimeric RNA-DNA hairpin targeting the same sequence alteration. Moreover, the efficiency of sequence alteration or gene conversion directed by an unmodified oligonucleotide is many times lower as compared to a control chimeric RNA-DNA molecule or the modified oligonucleotides of the invention targeting the

same sequence alteration. Similarly, molecules containing at least 3 2'-O-methyl base analogs are about four to five fold less efficient as compared to an oligonucleotide having the same number of phosphorothioate linkages.

The oligonucleotides of the present invention for alteration of a single base are about 17 to about 121 nucleotides in length, preferably about 17 to about 74 nucleotides in length. Most preferably, however, the oligonucleotides of the present invention are at least about 25 bases in length, unless there are self-dimerization structures within the oligonucleotide. If the oligonucleotide has such an unfavorable structure, lengths longer than 35 bases are preferred. Oligonucleotides with modified ends both shorter and longer than certain of the exemplified, modified oligonucleotides herein function as gene repair or gene knockout agents and are within the scope of the present invention.

Once an oligomer is chosen, it can be tested for its tendency to self-dimerize, since self-dimerization may result in reduced efficiency of alteration of genetic information. Checking for self-dimerization tendency can be accomplished manually or, preferably, using a software program. One such program is Oligo Analyzer 2.0, available through Integrated DNA Technologies (Coralville, IA 52241) (http://www.idtdna.com); this program is available for use on the world wide web at

http://www.idtdna.com/program/oligoanalyzer/
oligoanalyzer.asp.

For each oligonucleotide sequence input into the program, Oligo Analyzer 2.0 reports possible self-dimerized duplex forms, which are usually only partially duplexed, along with the free energy change associated with such self-dimerization. Delta G-values that are negative and large in magnitude, indicating strong self-dimerization potential, are automatically flagged by the software as "bad". Another software program that analyzes oligomers for pair dimer formation is Primer Select from DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715, Phone: (608) 258-7420 (http://www.dnastar.com/products/PrimerSelect.html).

If the sequence is subject to significant self-dimerization, the addition of further sequence flanking the "repair" nucleotide can improve gene correction frequency.

Generally, the oligonucleotides of the present invention are identical in sequence to one strand of the target DNA, which can be either strand of the target DNA, with the exception of one or more targeted bases positioned within the DNA domain of the oligonucleotide, and preferably toward the middle between the modified terminal regions. Preferably, the difference in sequence of the oligonucleotide as compared to the targeted genomic DNA is located at about the middle of the oligonucleotide sequence. In a preferred embodiment, the oligonucleotides of the invention are complementary to the non-transcribed

strand of a duplex. In other words, the preferred oligonucleotides target the sense strand of the DNA, i.e. the oligonucleotides of the invention are preferably complementary to the strand of the target DNA the sequence of which is found in the mRNA.

The oligonucleotides of the invention can include more than a single base change. In an oligonucleotide that is about a 70-mer, with at least one modified residue incorporated on the ends, as disclosed herein, multiple bases can be simultaneously targeted for change. The target bases may be up to 27 nucleotides apart and may not be changed together in all resultant plasmids in all cases. There is a frequency distribution such that the closer the target bases are to each other in the central DNA domain within the oligonucleotides of the invention, the higher the frequency of change in a given cell. Target bases only two nucleotides apart are changed together in every case that has been analyzed. The farther apart the two target bases are, the less frequent the simultaneous change. Thus, oligonucleotides of the invention may be used to repair or alter multiple bases rather than just one single base. For example, in a 74-mer oligonucleotide having a central base targeted for change, a base change event up to about 27 nucleotides away can also be effected. The positions of the altering bases within the oligonucleotide can be optimized using any one of the assays described herein. Preferably, the altering bases are at least about 8 nucleotides from one end of the oligonucleotide.

The oligonucleotides of the present invention can be introduced into cells by any suitable means. According to certain preferred embodiments, the modified oligonucleotides may be used alone. Suitable means, however, include the use of polycations, cationic lipids, liposomes, polyethylenimine (PEI), electroporation, biolistics, microinjection and other methods known in the art to facilitate cellular uptake. For plant cells, biolistic or particle bombardment methods are typically used. According to certain preferred embodiments of the present invention, isolated plant cells are treated in culture according to the methods of the invention, to mutate or repair a target gene. Alternatively, plant target DNA may be modified *in vitro* or in another cell type, including for example, yeast or bacterial cells and then introduced into a plant cell as, for example, a T-DNA. Plant cells thus modified may be used to regenerate the whole organism as, for example, in a plant having a desired targeted genomic change. In other instances, targeted genomic alteration, including repair or mutagenesis, may take place *in vivo* following direct administration of the modified, single-stranded oligonucleotides of the invention to a subject.

The single-stranded, modified oligonucleotides of the present invention have numerous applications as gene repair, gene modification, or gene knockout agents. Such oligonucleotides may be advantageously used, for example, to introduce or correct multiple point mutations. Each mutation leads to the addition, deletion or substitution of at least one base pair. The methods of the present invention

offer distinct advantages over other methods of altering the genetic makeup of an organism, in that only the individually targeted bases are altered. No additional foreign DNA sequences are added to the genetic complement of the organism. Such agents may, for example, be used to develop plants with improved traits by rationally changing the sequence of selected genes in isolated cells and using these modified cells to regenerate whole plants having the altered gene. See, e.g., U.S. Patent 6,046,380 and U.S. Patent 5,905,185 incorporated herein by reference. Such plants produced using the compositions of the invention lack additional undesirable selectable markers or other foreign DNA sequences. Targeted base pair substitution or frameshift mutations introduced by an oligonucleotide in the presence of a cell-free extract also provides a way to modify the sequence of extrachromosomal elements, including, for example, plasmids, cosmids and artificial chromosomes. The oligonucleotides of the invention also simplify the production of plants having particular modified or inactivated genes. Altered plant model systems such as those produced using the methods and oligonucleotides of the invention are invaluable in determining the function of a gene and in evaluating drugs. The oligonucleotides and methods of the present invention may also be used to introduce molecular markers, including, for example, SNPs, RFLPs, AFLPs and CAPs.

The purified oligonucleotide compositions may be formulated in accordance with routine procedures depending on the target. For example, purified oligonucleotide can be used directly in a standard reaction mixture to introduce alterations into targeted DNA *in vitro* or where cells are the target as a composition adapted for bathing cells in culture or for microinjection into cells in culture. The purified oligonucleotide compositions may also be provided on coated microbeads for biolistic delivery into plant cells. Where necessary, the composition may also include a solubilizing agent. Generally, the ingredients will be supplied either separately or mixed together in single-use form, for example, as a dry, lyophilized powder or water-free concentrate. In general, dosage required for efficient targeted gene alteration will range from about 0.001 to 50,000 μg/kg target tissue, preferably between 1 to 250 μg/kg, and most preferably at a concentration of between 30 and 60 micromolar.

For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In a preferred method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim) or an equivalent such as lipofectin. The amount of the oligonucleotide used is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells. For electroporation, between 20 and 2000 nanograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve

efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein. For biolistic delivery, microbeads are generally coated with resuspended oligonucleotides, which range of oligonucleotide to microbead concentration can be similarly adjusted to improve efficiency as determined using one of the assay methods described herein, starting with about 0.05 to 1 microgram of oligonucleotide to 25 microgram of 1.0 micrometer gold beads or similar microcarrier.

Another aspect of the invention is a kit comprising at least one oligonucleotide of the invention. The kit may comprise an additional reagent or article of manufacture. The additional reagent or article of manufacture may comprise a delivery mechanism, cell extract, a cell, or a plasmid, such as one of those disclosed in the Figures herein, for use in an assay of the invention. Alternatively, the invention includes a kit comprising an isogenic set of cells in which each cell in the kit comprises a different altered amino acid for a target protein encoded by a targeted altered gene within the cell produced according to the methods of the invention.

Brief Description Of The Drawings

Figure 1. *Flow diagram for the generation of modified single-stranded oligonucleotides.* The upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (A) 2'-O-methyl RNA nucleotides or (B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. HUH7 cells are described in Nakabayashi et al., Cancer Research 42: 3858-3863 (1982). Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene. The numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the molecule. Hence oligo 12S/25G contains an all phosphorothioate backbone, displayed as a dotted line. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G). Figure 1(C) provides a schematic plasmid indicating the sequence of the kan chimeric double-stranded hairpin oligonucleotide (left) and the sequence the tet chimeric double-stranded hairpin oligonucleotide used in other experiments. Figure 1(D) provides a flow chart of a kan experiment in which a chimeric double-stranded hairpin oligonucleotide is used.

Figure 2. *Genetic readout system for correction of a point mutation in plasmid* pK^{s}m4021. A mutant kanamycin gene harbored in plasmid pK^{s}m4021 is the target for correction by oligonucleotides.

The mutant G is converted to a C by the action of the oligo. Corrected plasmids confer resistance to kanamycin in *E.coli* (DH10B) after electroporation leading to the genetic readout and colony counts.

Figure 3: *Target plasmid and sequence correction of a frameshift mutation by chimeric and single-stranded oligonucleotides.* (A) Plasmid pT$^s\Delta$208 contains a single base deletion mutation at position 208 rendering it unable to confer tet resistance. The target sequence presented below indicates the insertion of a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) DNA sequence confirming base insertion directed by Tet 3S/25G; the yellow highlight indicates the position of frameshift repair.

Figure 4. *DNA sequences of representative kan^r colonies.* Confirmation of sequence alteration directed by the indicated molecule is presented along with a table outlining codon distribution. Note that 10S/25G and 12S/25G elicit both mixed and unfaithful gene repair. The number of clones sequenced is listed in parentheses next to the designation for the single-stranded oligonucleotide. A plus (+) symbol indicates the codon identified while a figure after the (+) symbol indicates the number of colonies with a particular sequence. TAC/TAG indicates a mixed peak. Representative DNA sequences are presented below the table with yellow highlighting altered residues.

Figure 5. *Gene correction in HeLa cells.* Representative oligonucleotides of the invention are co-transfected with the pCMVneo(')FIAsH plasmid (shown in Figure 9) into HeLa cells. Ligand is diffused into cells after co-transfection of plasmid and oligonucleotides. Green fluorescence indicates gene correction of the mutation in the antibiotic resistance gene. Correction of the mutation results in the expression of a fusion protein that carries a marker ligand binding site and when the fusion protein binds the ligand, a green fluorescence is emitted. The ligand is produced by Aurora Biosciences and can readily diffuse into cells enabling a measurement of corrected protein function; the protein must bind the ligand directly to induce fluorescence. Hence cells bearing the corrected plasmid gene appear green while "uncorrected" cells remain colorless.

Figure 6. *Z-series imaging of corrected cells.* Serial cross-sections of the HeLa cell represented in Figure 5 are produced by Zeiss 510 LSM confocal microscope revealing that the fusion protein is contained within the cell.

Figure 7. *Hygromycin-eGFP target plasmids.* (A) Plasmid pAURHYG(ins)GFP contains a single base insertion mutation between nucleotides 136 and 137, at codon 46, of the Hygromycin B coding sequence (cds) which is transcribed from the constitutive ADH1 promoter. The target sequence presented below indicates the deletion of an A and the substitution of a C for a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) Plasmid pAURHYG(rep)GFP contains a

base substitution mutation introducing a G at nucleotide 137, at codon 46, of the Hygromycin B coding sequence (cds). The target sequence presented below the diagram indicates the amino acid conservative replacement of G with C, restoring gene function.

Figure 8. *Oligonucleotides for correction of hygromycin resistance gene.* The sequence of the oligonucleotides used in experiments to assay correction of a hygromycin resistance gene are shown. DNA residues are shown in capital letters, RNA residues are shown in lowercase and nucleotides with a phosphorothioate backbone are capitalized and underlined.

Figure 9. *pAURNeo(-)FlAsH plasmid.* This figure describes the plasmid structure, target sequence, oligonucleotides, and the basis for detection of the gene alteration event by fluorescence.

Figure 10. pYESHyg(x)eGFP plasmid. This plasmid is a construct similar to the pAURHyg(x)eGFP construct shown in Figure 7, except the promoter is the inducible GAL1 promoter. This promoter is inducible with galactose, leaky in the presence of raffinose, and repressed in the presence of dextrose.

Figure 11. pBI-HygeGFP plasmid. This plasmid is a construct based on the plasmids pBI101, pBI 101.2, pBI101.3 or pBI 121 available from Clontech in which HygeGFP replaces the beta-glucuronidase gene of the Clontech plasmids. The different Clontech plasmids vary by a reading frame shift relative to the polylinker, or the presence of the Cauliflower mosaic virus promoter.

The following examples are provided by way of illustration only, and are not intended to limit the scope of the invention disclosed herein.

EXAMPLE 1
Assay Method For Base Alteration And Preferred Oligonucleotide Selection

In this example, single-stranded and double-hairpin oligonucleotides with chimeric backbones (see Figure 1 for structures (A and B) and sequences (C and D) of assay oligonucleotides) are used to correct a point mutation in the kanamycin gene of $pK^{s}m4021$ (Figure 2) or the tetracycline gene of $pT^{s}\Delta208$ (Figure 3). All kan oligonucleotides share the same 25 base sequence surrounding the target base identified for change, just as all tet oligonucleotides do. The sequence is given in Figures 1C and Figure 1D. Each plasmid contains a functional ampicillin gene. Kanamycin gene function is restored when a G at position 4021 is converted to a C (via a substitution mutation); tetracycline gene function is restored when a deletion at position 208 is replaced by a C (via frameshift mutation). A separate plasmid, pAURNeo(-)FlAsH (Figure 9), bearing the kan^{s} gene is used in the cell culture experiments. This plasmid was constructed by inserting a synthetic expression cassette containing a neomycin phosphotransferase

(kanamycin resistance) gene and an extended reading frame that encodes a receptor for the FlAsH ligand into the pAUR123 shuttle vector (Panvera Corp., Madison, WI). The resulting construct replicates in *S. cerevisiae* at low copy number, confers resistance to aureobasidinA and constitutively expresses either the Neo+/FlAsH fusion product (after alteration) or the truncated Neo-/FlAsH product (before alteration) from the ADH1 promoter. By extending the reading frame of this gene to code for a unique peptide sequence capable of binding a small ligand to form a fluorescent complex, restoration of expression by correction of the stop codon can be detected in real time using confocal microscopy.

Additional constructs can be made to test additional gene alteration events or for specific use in different expression systems. For example, alternative comparable plant plasmids or integration vectors such as, e.g. those based on T-DNA, can be constructed for stable expression in plant cells according to the disclosures herein. Such constructs would use a plant specific promoter such as, e.g., cauliflower mosaic virus 35S promoter, to replace the promoters directing expression of the neo, hyg or aureobasidinA resistance gene disclosed herein, including for example, in Figures 7B, 9 and 10 herein. Moreover, the green fluorescent protein (GFP) sequence used herein may be modified to increase expression in plant cells such as Arabidopsis and the other plants disclosed herein as described in Haseloff et al., Proc. Natl.Acad. Sci. 94(6): 2122-7 (1997), Rouwendal et al. Plant Mol. Biol. 33(6): 989-99 (1997) and Hu et al. FEBS Lett. 369(2-3): 331-4 (1995). Codon usage for optimal expression of GFP in plants results from increasing the frequency of codons with a C or a G in the third position from 32 to about 60%. Specific constructs are disclosed and can be used as follows with such plant specific alterations.

We also construct three mammalian expression vectors, pHyg(rep)eGFP, pHyg(Δ)eGFP, pHyg(ins)eGFP, that contain a substitution mutation at nucleotide 137 of the hygromycin-B coding sequence. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. All point mutations create a nonsense termination codon at residue 46. We use pHYGeGFP plasmid (Invitrogen, CA) DNA as a template to introduce the mutations into the hygromycin-eGFP fusion gene by a two step site-directed mutagenesis PCR protocol. First, we generate overlapping 5' and a 3' amplicons surrounding the mutation site by PCR for each of the point mutation sites. A 215 bp 5' amplicon for the (rep), (Δ) or (ins) was generated by polymerization from oligonucleotide primer HygEGFPf (5'-AATACGACTCACTATAGG-3') to primer Hygrepr (5'GACCTATCCACGCCCTCC-3'), HygΔr (5'-GACTATCCACGCCCTCC-3'), or Hyginsr (5'-GACATTATCCACGCCCTCC-3'), respectively. We generate a 300bp 3' amplicon for the (rep), (Δ) or (ins) by polymerization from oligonucleotide primers Hygrepf (5'-CTGGGATAGGTCCTGCGG-3'), HygΔf

(5'-CGTGGATAGTCCTGCGG-3'), Hyginsf (5'-CGTGGATAATGTCCTGCGG-3'), respectively to primer HygEGFPr (5'-AAATCACGCCATGTAGTG-3'). We mix 20 ng of each of the resultant 5' and 3' overlapping amplicon mutation sets and use the mixture as a template to amplify a 523 bp fragment of the Hygromycin gene spanning the KpnI and RsrII restriction endonuclease sites. We use the Expand PCR system (Roche) to generate all amplicons with 25 cycles of denaturing at 94°C for 10 seconds, annealing at 55°C for 20 seconds and elongation at 68°C for 1 minute. We digest 10 μg of vector pHYGeGFP and 5 μg of the resulting fragments for each mutation with KpnI and RsrII (NEB) and gel purify the fragment for enzymatic ligation. We ligate each mutated insert into pHYGeGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm the mutation by Sanger dideoxy chain termination sequencing and purify the plasmid using a Qiagen maxiprep kit.

Oligonucleotide synthesis and cells. Chimeric oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) are synthesized using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, each oligonucleotide is gel-purified using, for example, procedures such as those described in Gamper *et al.*, *Biochem.* 39, 5808-5816 (2000) and the concentrations determined spectrophotometrically (33 or 40 μg/ml per A_{260} unit of single-stranded or hairpin oligomer). HUH7 cells are grown in DMEM, 10% FBS, 2mM glutamine, 0.5% pen/strep. The *E.coli* strain, DH10B, is obtained from Life Technologies (Gaithersburg, MD); DH10B cells contain a mutation in the RECA gene (*recA*).

Cell-free extracts. Although this portion of this example is directed to mammalian systems, similar extracts from plants can be prepared as disclosed elsewhere in this application and used as disclosed in this example. We prepare cell-free extracts from HUH7 cells or other mammalian cells, as follows. We employ this protocol with essentially any mammalian cell including, for example, H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C127I (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma). We harvest approximately $2x10^8$ cells. We then wash the cells immediately in cold hypotonic buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM $MgCl_2$; 1 mM DTT) with 250 mM sucrose. We then resuspend the cells in cold hypotonic buffer without sucrose and after 15 minutes we lyse the cells with 25 strokes of a Dounce homogenizer using a tight fitting pestle. We incubate the lysed cells for 60 minutes on ice and centrifuge the sample for 15 minutes at 12000x*g*. The cytoplasmic fraction is enriched with nuclear proteins due to the extended co-incubation of the fractions following cell breakage.

We then immediately aliquote and freeze the supernatant at -80°C. We determine the protein concentration in the extract by the Bradford assay.

We also perform these experiments with cell-free extracts obtained from fungal cells, including, for example, *S. cerevisiae* (yeast), *Ustilago maydis*, and *Candida albicans*. For example, we grow yeast cells into log phase in 2L YPD medium for 3 days at 30°C. We then centrifuge the cultures at 5000x*g*, resuspend the pellets in a 10% sucrose, 50 mM Tris, 1mM EDTA lysis solution and freeze them on dry ice. After thawing, we add KCl, spermidine and lyticase to final concentrations of 0.25 mM, 5 mM and 0.1 mg/ml, respectively. We incubate the suspension on ice for 60 minutes, add PMSF and Triton X100 to final concentrations of 0.1 mM and 0.1% and continue to incubate on ice for 20 minutes. We centrifuge the lysate at 3000x*g* for 10 minutes to remove larger debris. We then remove the supernatant and clarify it by centrifuging at 30000x*g* for 15 minutes. We then add glycerol to the clarified extract to a concentration of 10% (v/v) and freeze aliquots at -80°C. We determine the protein concentration of the extract by the Bradford assay.

Reaction mixtures of 50 µl are used, consisting of 10-30 µg protein of cell-free extract, which can be optionally substituted with purified proteins or enriched fractions, about 1.5 µg chimeric double-hairpin oligonucleotide or 0.55 µg single-stranded molecule (3S/25G or 6S/25G, see Figure 1), and 1 µg of plasmid DNA (see Figures 2 and 3) in a reaction buffer of 20 mM Tris, pH 7.4, 15 mM $MgCl_2$, 0.4 mM DTT, and 1.0 mM ATP. Reactions are initiated with extract and incubated at 30°C for 45 min. The reaction is stopped by placing the tubes on ice and then immediately deproteinized by two phenol/chloroform (1:1) extractions. Samples are then ethanol precipitated. The nucleic acid is pelleted at 15,000 r.p.m. at 4°C for 30 min., is washed with 70% ethanol, resuspended in 50 µl H_2O, and is stored at -20°C. 5 µl of plasmid from the resuspension (~100 ng) was transfected in 20 µl of DH10B cells by electroporation (400 V, 300 µF, 4 kΩ) in a Cell-Porator apparatus (Life Technologies). After electroporation, cells are transferred to a 14 ml Falcon snap-cap tube with 2 ml SOC and shaken at 37°C for 1 h. Enhancement of final kan colony counts is achieved by then adding 3 ml SOC with 10 µg/ml kanamycin and the cell suspension is shaken for a further 2 h at 37°C. Cells are then spun down at 3750 x g and the pellet is resuspended in 500 µl SOC. 200 µl is added undiluted to each of two kanamycin (50 µg/ml) agar plates and 200 µl of a 10^5 dilution is added to an ampicillin (100 µg/ml) plate. After overnight 37°C incubation, bacterial colonies are counted using an Accucount 1000 (Biologics). Gene conversion effectiveness is measured as the ratio of the average of the kan colonies on both plates per amp colonies multiplied by 10^{-5} to correct for the amp dilution.

The following procedure can also be used. 5 μl of resuspended reaction mixtures (total volume 50 μl) are used to transform 20 μl aliquots of electro-competent DH10B bacteria using a Cell-Porator apparatus (Life Technologies). The mixtures are allowed to recover in 1 ml SOC at 37°C for 1 hour at which time 50 μg/ml kanamycin or 12 μg/ml tetracycline is added for an additional 3 hours. Prior to plating, the bacteria are pelleted and resuspended in 200 μ1 of SOC. 100 μl aliquots are plated onto kan or tet agar plates and 100 μl of a 10^{-4} dilution of the cultures are concurrently plated on agar plates containing 100 μg/ml of ampicillin. Plating is performed in triplicate using sterile Pyrex beads. Colony counts are determined by an Accu-count 1000 plate reader (Biologics). Each plate contains 200-500 ampicillin resistant colonies or 0-500 tetracycline or kanamycin resistant colonies. Resistant colonies are selected for plasmid extraction and DNA sequencing using an ABI Prism kit on an ABI 310 capillary sequencer (PE Biosystems).

Chimeric single-stranded oligonucleotides. In Figure 1 the upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (Figure 1A) 2'-O-methyl RNA nucleotides or (Figure 1B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene.

Molecules bearing 3, 6, 8, 10 and 12 phosphorothioate linkages in the terminal regions at each end of a backbone with a total of 24 linkages (25 bases) are tested in the kan^s system. Alternatively, molecules bearing 2, 4, 5, 7, 9 and 11 in the terminal regions at each end are tested. The results of one such experiment, presented in Table 1 and Figure 1B, illustrate an enhancement of correction activity directed by some of these modified structures. In this illustrative example, the most efficient molecules contained 3 or 6 phosphorothioate linkages at each end of the 25-mer; the activities are approximately equal (molecules IX and X with results of 3.09 and 3.7 respectively). A reduction in alteration activity may be observed as the number of modified linkages in the molecule is further increased. Interestingly, a single-strand molecule containing 24 phosphorothioate linkages is minimally active suggesting that this backbone modification when used throughout the molecule supports only a low level of targeted gene repair or alteration. Such a non-altering, completely modified molecule can provide a baseline control for determining efficiency of correction for a specific oligonucleotide molecule of known sequence in defining the optimum oligonucleotide for a particular alteration event.

The efficiency of gene repair directed by phosphorothioate-modified, single-stranded molecules, in a length dependent fashion, led us to examine the length of the RNA modification used in

the original chimera as it relates to correction. Construct III represents the "RNA-containing" strand of chimera I and, as shown in Table 1 and Figure 2A, it promotes inefficient gene repair. But, as shown in the same figure, reducing the RNA residues on each end from 10 to 3 increases the frequency of repair. At equal levels of modification, however, 25-mers with 2'-O-methyl ribonucleotides were less effective gene repair agents than the same oligomers with phosphorothioate linkages. These results reinforce the fact that an RNA containing oligonucleotide is not as effective in promoting gene repair or alteration as a modified DNA oligonucleotide.

Repair of the kanamycin mutation requires a G→C exchange. To confirm that the specific desired correction alteration was obtained, colonies selected at random from multiple experiments are processed and the isolated plasmid DNA is sequenced. As seen in Figure 4, colonies generated through the action of the single-stranded molecules 3S/25G (IX), 6S/25G (X) and 8S/25G (XI) respectively contained plasmid molecules harboring the targeted base correction. While a few colonies appeared on plates derived from reaction mixtures containing 25-mers with 10 or 12 thioate linkages on both ends, the sequences of the plasmid molecules from these colonies contain nonspecific base changes. In these illustrative examples, the second base of the codon is changed (see Figure 3). These results show that modified single-strands can direct gene repair, but that efficiency and specificity are reduced when the 25-mers contain 10 or more phosphorothioate linkages at each end.

In Figure 1, the numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the examplified molecule although other molecules with 2, 4, 5, 7, 9 and 11 modifications at each end can also be tested. Hence oligo 12S/25G represents a 25-mer oligonucleotide which contains 12 phosphorothioate linkages on each side of the central G target mismatch base producing a fully phosphorothioate linked backbone, displayed as a dotted line. The dots are merely representative of a linkage in the figure and do not depict the actual number of linkages of the oligonucleotide. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G).

Correction of a mutant kanamycin gene in cultured mammalian cells. Although this portion of this example is directed to cultured mammalian cells, comparable methods may be used using cultured plant cells or protoplasts of those cells from the plant species disclosed herein. The experiments are performed using different eukaryotic cells including plant and mammalian cells, including, for example, 293 cells (transformed human primary kidney cells), HeLa cells (human cervical carcinoma), and H1299 (human epithelial carcinoma, non-small cell lung cancer). HeLa cells are grown at 37°C and 5% CO_2 in a humidified incubator to a density of 2×10^5 cells/ml in an 8 chamber slide (Lab-Tek). After replacing the

regular DMEM with Optimem, the cells are co-transfected with 10 μg of plasmid pAURNeo(-)FlAsH and 5 μg of modified single-stranded oligonucleotide (3S/25G) that is previously complexed with 10 μg lipofectamine, according to the manufacturer's directions (Life Technologies). The cells are treated with the liposome-DNA-oligo mix for 6 hrs at 37°C. Treated cells are washed with PBS and fresh DMEM is added. After a 16-18 hr recovery period, the culture is assayed for gene repair. The same oligonucleotide used in the cell-free extract experiments is used to target transfected plasmid bearing the kan^s gene. Correction of the point mutation in this gene eliminates a stop codon and restores full expression. This expression can be detected by adding a small non-fluorescent ligand that bound to a C-C-R-E-C-C sequence in the genetically modified carboxy terminus of the kan protein, to produce a highly fluorescent complex (FlAsH system, Aurora Biosciences Corporation). Following a 60 min incubation at room temperature with the ligand (FlAsH-EDT2), cells expressing full length kan product acquire an intense green fluorescence detectable by fluorescence microscopy using a fluorescein filter set. Similar experiments are performed using the HygeGFP target as described in Example 2 with a variety of mammalian cells, including, for example, COS-1 and COS-7 cells (African green monkey), and CHO-K1 cells (Chinese hamster ovary). The experiments are also performed with PG12 cells (rat pheochromocytoma) and ES cells (human embryonic stem cells).

Summary of experimental results. Tables 1, 2 and 3 respectively provide data on the efficiency of gene repair directed by single-stranded oligonucleotides. Table 1 presents data using a cell-free extract from human liver cells (HUH7) to catalyze repair of the point mutation in plasmid $pkan^s m4021$ (see Figure 1). Table 2 illustrates that the oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity. Table 3 illustrates data from the repair of a frameshift mutation (Figure 3) in the tet gene contained in plasmid pTetΔ208. Table 4 illustrates data from repair of the $pkan^s m4021$ point mutation catalyzed by plant cell extracts prepared from canola and musa (banana). Colony numbers are presented as kan^r or tet^r and fold increases (single strand versus double hairpin) are presented for kan^r in Table 1.

Figure 5A is a confocal picture of HeLa cells expressing the corrected fusion protein from an episomal target. Gene repair is accomplished by the action of a modified single-stranded oligonucleotide containing 3 phosphorothioate linkages at each end (3S/25G). Figure 5B represents a "Z-series" of HeLa cells bearing the corrected fusion gene. This series sections the cells from bottom to top and illustrates that the fluorescent signal is "inside the cells".

Results. In summary, we have designed a novel class of single-stranded oligonucleotides with backbone modifications at the termini and demonstrate gene repair/conversion

activity in mammalian and plant cell-free extracts. We confirm that the all DNA strand of the RNA-DNA double-stranded double hairpin chimera is the active component in the process of gene repair. In some cases, the relative frequency of repair by the novel oligonucleotides of the invention is elevated approximately 3-4-fold in certain embodiments when compared to frequencies directed by chimeric RNA-DNA double hairpin oligonucleotides.

This strategy centers around the use of extracts from various sources to correct a mutation in a plasmid using a modified single-stranded or a chimeric RNA-DNA double hairpin oligonucleotide. A mutation is placed inside the coding region of a gene conferring antibiotic resistance in bacteria, here kanamycin or tetracycline. The appearance of resistance is measured by genetic readout in *E.coli* grown in the presence of the specified antibiotic. The importance of this system is that both phenotypic alteration and genetic inheritance can be measured. Plasmid pK^{s}m4021 contains a mutation (T→G) at residue 4021 rendering it unable to confer antibiotic resistance in *E.coli*. This point mutation is targeted for repair by oligonucleotides designed to restore kanamycin resistance. To avoid concerns of plasmid contamination skewing the colony counts, the directed correction is from G→C rather than G→T (wild-type). After isolation, the plasmid is electroporated into the DH10B strain of *E.coli*, which contains inactive RecA protein. The number of kanamycin colonies is counted and normalized by ascertaining the number of ampicillin colonies, a process that controls for the influence of electroporation. The number of colonies generated from three to five independent reactions was averaged and is presented for each experiment. A fold increase number is recorded to aid in comparison.

The original RNA-DNA double hairpin chimera design, e.g., as disclosed in U.S. Patent 5,565,350, consists of two hybridized regions of a single-stranded oligonucleotide folded into a double hairpin configuration. The double-stranded targeting region is made up of a 5 base pair DNA/DNA segment bracketed by 10 base pair RNA/DNA segments. The central base pair is mismatched to the corresponding base pair in the target gene. When a molecule of this design is used to correct the kan^s mutation, gene repair is observed (I in Figure 1A). Chimera II (Figure 1B) differs partly from chimera I in that only the DNA strand of the double hairpin is mismatched to the target sequence. When this chimera was used to correct the kan^s mutation, it was twice as active. In the same study, repair function could be further increased by making the targeting region of the chimera a continuous RNA/DNA hybrid.

Frame shift mutations are repaired. By using plasmid pT^{s}Δ208, described in Figure 1(C) and Figure 3, the capacity of the modified single-stranded molecules that showed activity in correcting a point mutation, can be tested for repair of a frameshift. To determine efficiency of correction of the mutation, a chimeric oligonucleotide (Tet I), which is designed to insert a T residue at position 208, is

used. A modified single-stranded oligonucleotide (Tet IX) directs the insertion of a T residue at this same site. Figure 3 illustrates the plasmid and target bases designated for change in the experiments. When all reaction components are present (extract, plasmid, oligomer), tetracycline resistant colonies appear. The colony count increases with the amount of oligonucleotide used up to a point beyond which the count falls off (Table 3). No colonies above background are observed in the absence of either extract or oligonucleotide, nor when a modified single-stranded molecule bearing perfect complementarity is used. Figure 3 represents the sequence surrounding the target site and shows that a T residue is inserted at the correct site. We have isolated plasmids from fifteen colonies obtained in three independent experiments and each analyzed sequence revealed the same precise nucleotide insertion. These data suggest that the single-stranded molecules used initially for point mutation correction can also repair nucleotide deletions.

Comparison of phosphorothioate oligonucleotides to 2'-O-methyl substituted oligonucleotides. From a comparison of molecules VII and XI, it is apparent that gene repair is more subject to inhibition by RNA residues than by phosphorothioate linkages. Thus, even though both of these oligonucleotides contain an equal number of modifications to impart nuclease resistance, XI (with 16 phosphorothioate linkages) has good gene repair activity while VII (with 16 2'-O-methyl RNA residues) is inactive. Hence, the original chimeric double hairpin oligonucleotide enabled correction directed, in large part, by the strand containing a large region of contiguous DNA residues.

Oligonucleotides can target multiple nucleotide alterations within the same template. The ability of individual single-stranded oligonucleotides to correct multiple mutations in a single target template is tested using the plasmid pK^{s}m4021 and the following single-stranded oligonucleotides modified with 3 phosphorothioate linkages at each end (indicated as underlined nucleotides): Oligo1 is a 25-mer with the sequence TTCGATAAGCCTATGCTGACCCGTG corrects the original mutation present in the kanamycin resistance gene of pK^{s}m4021 as well as directing another alteration 2 basepairs away in the target sequence (both indicated in boldface); Oligo2 is a 70-mer with the 5'-end sequence TTCGGCTACGACTGGGCACAACAGACAATTGGC with the remaining nucleotides being completely complementary to the kanamycin resistance gene and also ending in 3 phosphorothioate linkages at the 3' end. Oligo2 directs correction of the mutation in pK^{s}m4021 as well as directing another alteration 21 basepairs away in the target sequence (both indicated in boldface).

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pK^{s}M4021 plasmid. These include, for example, a second 25-mer that alters two nucleotides that are three nucleotides apart with the sequence 5'-

TTGTGCCCAGTC**G**TA**T**CCGAATAGC-3'; a 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-CATCAGAGCAGCC**A**ATTGTCTGTTGTGCCCAGTC**G**TAGCCGAA TAGCCTCTCCACCCAAGCGGCCGGAGA-3'; and another 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-GCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC**A**ATTGTCTGTTGTGCCCAGTC**G**TAGCCGAAT AGCCT-3'. The nucleotides in the oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same way as the other oligonucleotides of the invention.

We assay correction of the original mutation in pK^{s}m4021 by monitoring kanamycin resistance (the second alterations which are directed by Oligo2 and Oligo3 are silent with respect to the kanamycin resistance phenotype). In addition, in experiments with Oligo2, we also monitor cleavage of the resulting plasmids using the restriction enzyme Tsp509I which cuts at a specific site present only when the second alteration has occurred (at ATT in Oligo2). We then sequence these clones to determine whether the additional, silent alteration has also been introduced. The results of an analysis are presented below:

	Oligo1 (25-mer)	Oligo2 (70-mer)
Clones with both sites changed	9	7
Clones with a single site changed	0	2
Clones that were not changed	4	1

Nuclease sensitivity of unmodified DNA oligonucleotide. Electrophoretic analysis of nucleic acid recovered from the cell-free extract reactions conducted here confirm that the unmodified single-stranded 25-mer did not survive incubation whereas greater than 90% of the terminally modified oligos did survive (as judged by photo-image analyses of agarose gels).

Plant extracts direct repair. The modified single-stranded constructs can be tested in plant cell extracts. We have observed gene alteration using extracts from multiple plant sources, including, for example, Arabidopsis, tobacco, banana, maize, soybean, canola, wheat, spinach as well as spinach chloroplast extract or extracts made from other plant cells disclosed herein. We prepare the extracts by grinding plant tissue or cultured cells under liquid nitrogen with a mortar and pestle. We extract 3 ml of the ground plant tissue with 1.5 ml of extraction buffer (20 mM HEPES, pH7.5; 5 mM KCl;

1.5 mM $MgCl_2$; 10 mM DTT; and 10% [v/v] glycerol). Some plant cell-free extracts also include about 1% (w/v) PVP. We then homogenize the samples with 15 strokes of a Dounce homogenizer. Following homogenization, we incubate the samples on ice for 1 hour and centrifuge at 3000 x *g* for 5 minutes to remove plant cell debris. We then determine the protein concentration in the supernatants (extracts) by Bradford assay. We dispense 100 µg (protein) aliquots of the extracts which we freeze in a dry ice-ethanol bath and store at -80°C.

We describe experiments using two sources here: a dicot (canola) and a monocot (banana, *Musa acuminata* cv. Rasthali). Each vector directs gene repair of the kanamycin mutation (Table 4); however, the level of correction is elevated 2-3 fold relative to the frequency observed with the chimeric oligonucleotide. These results are similar to those observed in the mammalian system wherein a significant improvement in gene repair occurred when modified single-stranded molecules were used.

Tables are attached hereto.

Table I

Gene repair activity is directed by single-stranded oligonucleotides.

Oligonucleotide	Plasmid	Extract (ug)	kan^r colonies	Fold increase
I	pK^{S}m4021	10	300	
I		20	418	1.0x
II		10	537	
II		20	748	1.78x
III		10	3	
III		20	5	0.01x
IV		10	112	
IV		20	96	0.22x
V		10	217	
V		20	342	0.81x
VI		10	6	
VI		20	39	0.093x
VII		10	0	
VII		20	0	0x
VIII		10	3	
VIII		20	5	0.01x
IX		10	936	
IX		20	1295	3.09x
X		10	1140	
X		20	1588	3.7x
XI		10	480	
XI		20	681	1.6x
XII		10	18	
XII		20	25	0.059x
XIII		10	0	
XIII		20	4	0.009x
-		20	0	
I		-	0	

Plasmid pK^{s}m4021 (1μg), the indicated oligonucleotide (1.5 μg chimeric oligonucleotide or 0.55 μg single-stranded oligonucleotide; molar ratio of oligo to plasmid of 360 to 1) and either 10 or 20 μg of HUH7 cell-free extract were incubated 45 min at 37°C. Isolated plasmid DNA was electroporated into *E. coli* (strain DH10B) and the number of kan^r colonies counted. The data represent the number of kanamycin resistant colonies per 10^6 ampicillin resistant colonies generated from the same reaction and is the average of three

experiments (standard deviation usually less than +/- 15%). Fold increase is defined relative to 418 kan^r colonies (second reaction) and in all reactions was calculated using the 20µg sample.

Table II

Modified single-stranded oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity.

A. Oligonucleotide	Plasmid	Extract	kan^r colonies
IX (3S/25G)		HUH7	637
X (6S/25G)		HUH7	836
IX		$MEF2^{-/-}$	781
X		$MEF2^{-/-}$	676
IX		$MEF3^{-/-}$	582
X		$MEF3^{-/-}$	530
IX		$MEF^{+/+}$	332
X		$MEF^{+/+}$	497
-		$MEF2^{-/-}$	10
-		$MEF3^{-/-}$	5
-		$MEF^{+/+}$	14

Chimeric oligonucleotide (1.5 μg) or modified single-stranded oligonucleotide (0.55 μg) was incubated with 1μg of plasmid pK^sm4021 and 20μg of the indicated extracts. MEF represents mouse embryonic fibroblasts with either MSH2 ($2^{-/-}$) or MSH3 ($3^{-/-}$) deleted. $MEF^{+/+}$ indicates wild-type mouse embryonic fibroblasts. The other reaction components were then added and processed through the bacterial readout system. The data represent the number of kanamycin resistant colonies per 10^6 ampicillin resistant colonies.

Table III

Frameshift mutation repair is directed by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	tet^r colonies
Tet IX (3S/25A; 0.5 µg)	$pT^s\Delta208$ (1µg)	-	0
-		20µg	0
Tet IX (0.5 µg)			48
Tet IX (1.5 µg)			130
Tet IX (2.0 µg)			68
Tet I (chimera; 1.5 µg)			48

Each reaction mixture contained the indicated amounts of plasmid and oligonucleotide. The extract used for these experiments came from HUH7 cells. The data represent the number of tetracycline resistant colonies per 10^6 ampicillin resistant colonies generated from the same reaction and is the average of 3 independent experiments. Tet I is a chimeric oligonucleotide and Tet IX is a modified single-stranded oligonucleotide that are designed to insert a T residue at position 208 of $pT^s\Delta208$. These oligonucleotides are equivalent to structures I and IX in Figure 2.

Table IV

Plant cell-free extracts support gene repair by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	kan^r colonies
II (chimera)	pK^Sm4021	30µg Canola	337
IX (3S/25G)		Canola	763
X (6S/25G)		Canola	882
II		*Musa*	203
IX		*Musa*	343
X		*Musa*	746
-		Canola	0
-		*Musa*	0
IX		- Canola	0
X		- *Musa*	0

Canola or Musa cell-free extracts were tested for gene repair activity on the kanamycin-sensitive gene as previously described in (18). Chimeric oligonucleotide II (1.5 µg) and modified single-stranded oligonucleotides IX and X (0.55µg) were used to correct pK^Sm4021. Total number of kan^r colonies are present per 10^7 ampicillin resistant colonies and represent an average of four independent experiments.

Table V

Gene repair activity in cell-free extracts prepared from yeast (Saccharomyces cerevisiae)

Cell-type	Plasmid	Chimeric Oligo	SS Oligo	$kan^r/amp^r \times 10^6$
Wild type	$pKan^s m4021$	1μg		0.36
Wild type			1μg	0.81
ΔRAD52		1μg		10.72
ΔRAD52			1μg	17.41
ΔPMS1		1μg		2.02
ΔPMS1			1μg	3.23

In this experiment, the kan^s gene in $pKan^s4021$ is corrected by either a chimeric double-hairpin oligonucleotide or a single-stranded oligonucleotide containing three thioate linkages at each end (3S/25G).

EXAMPLE 2
Yeast Cell Targeting Assay Method for Base Alteration and Preferred Oligonucleotide Selection

In this example, single-stranded oligonucleotides with modified backbones and double-hairpin oligonucleotides with chimeric, RNA-DNA backbones are used to measure gene repair using two episomal targets with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair. These plasmids are pAURHYG(rep)GFP, which contains a point mutation in the hygromycin resistance gene (Figure 7), pAURHYG(ins)GFP, which contains a single-base insertion in the hygromycin resistance gene (Figure 7) and pAURHYG(Δ)GFP which has a single base deletion. We also use the plasmid containing a wild-type copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)GFP, as a control. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, at codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In pAURHYG(ins)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, at codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene.

We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)EGFP and ligation into pAUR123 (Panvera, CA). We digest 10 μg pAUR123 vector DNA, as well as, 10 μg of each pHyg(x)EGFP construct with KpnI and SalI (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify using a Qiagen maxiprep kit.

We use this system to assay the ability of five oligonucleotides (shown in Figure 8) to support correction under a variety of conditions. The oligonucleotides which direct correction of the mutation in pAURHYG(rep)GFP can also direct correction of the mutation in pAURHYG(ins)GFP. Three of the four oligonucleotides (HygE3T/25, HygE3T/74 and HygGG/Rev) share the same 25-base sequence surrounding the base targeted for alteration. HygGG/Rev is an RNA-DNA chimeric double hairpin

oligonucleotide of the type described in the prior art. One of these oligonucleotides, HygE3T/74, is a 74-base oligonucleotide with the 25-base sequence centrally positioned. The fourth oligonucleotide, designated HygE3T/74α, is the reverse complement of HygE3T/74. The fifth oligonucleotide, designated Kan70T, is a non-specific, control oligonucleotide which is not complementary to the target sequence. Alternatively, an oligonucleotide of identical sequence but lacking a mismatch to the target or a completely thioate modified oligonucleotide or a completely 2-0-methylated modified oligonucleotide may be used as a control. Alternatively, oligonucleotides containing one, two, three, four, five, six, eight, ten or more LNA modifications on at least one of the two termini (and preferrably the 3' terminus) may be used in different embodiments.

Oligonucleotide synthesis and cells. We synthesized and purified the chimeric, double-hairpin oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) as described in Example 1. Plasmids used for assay were maintained stably in yeast (*Saccharomyces cerevisiae*) strain LSY678 *MATα* at low copy number under aureobasidin selection. Plasmids and oligonucleotides are introduced into yeast cells by electroporation as follows: to prepare electrocompetent yeast cells, we inoculate 10 ml of YPD media from a single colony and grow the cultures overnight with shaking at 300 rpm at 30°C. We then add 30 ml of fresh YPD media to the overnight cultures and continue shaking at 30°C until the OD_{600} was between 0.5 and 1.0 (3-5 hours). We then wash the cells by centrifuging at 4°C at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We then centrifuge at 4°C at 3000 rpm for 5 minutes and resuspend in 1 ml ice-cold 1M sorbitol and then finally centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the cells in 120 µl 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40 µl of cells with 5 µg of nucleic acid, unless otherwise stated, and incubate on ice for 5 minutes. We then transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene Pulser apparatus at 1.5 kV, 25 µF, 200 Ω for one five-second pulse. We then immediately resuspend the cells in 1 ml YPD supplemented with 1M sorbitol and incubate the cultures at 30°C with shaking at 300 rpm for 6 hours. We then spread 200 µl of this culture on selective plates containing 300 µg/ml hygromycin and spread 200 µl of a 10^5 dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We then count the colonies on the plates and calculate the gene conversion efficiency by determining the number of hygromycin resistance colonies per 10^5 aureobasidinA resistant colonies.

Frameshift mutations are repaired in yeast cells. We test the ability of the oligonucleotides shown in Figure 8 to correct a frameshift mutation *in vivo* using LSY678 yeast cells

containing the plasmid pAURHYG(ins)GFP. These experiments, presented in Table 6, indicate that these oligonucleotides can support gene correction in yeast cells. These data reinforce the results described in Example 1 indicating that oligonucleotides comprising phosphorothioate linkages facilitate gene correction much more efficiently than control duplex, chimeric RNA-DNA oligonucleotides. This gene correction activity is also specific as transformation of cells with the control oligonucleotide Kan70T produced no hygromycin resistant colonies above background and thus Kan70T did not support gene correction in this system. In addition, we observe that the 74-base oligonucleotide (HygE3T/74) corrects the mutation in pAURHYG(ins)GFP approximately five-fold more efficiently than the 25-base oligonucleotide (HygE3T/25). We also perform control experiments with LSY678 yeast cells containing the plasmid pAURHYG(wt)GFP. With this strain we observed that even without added oligonucleotides, there are too many hygromycin resistant colonies to count.

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pAURHYG(x)eGFP plasmid. These include, for example, one that alters two basepairs that are 3 nucleotides apart is a 74-mer with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGG**G**TA**C**GTCCTGCGGGTAAATAGCTGCGCCGATGGTTTCTAC-3'; a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATA**C**GTCCTGCGGGTAAA**C**AGCTGCGCCGATGGTTTCTAC-3'; and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATA**C**GTCCTGCGGGTAAATAGCTGCGCCGA**C**GGTTTCTAC. The nucleotides in these oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same ways as the other oligonucleotides of the invention.

Oligonucleotides targeting the sense strand direct gene correction more efficiently. We compare the ability of single-stranded oligonucleotides to target each of the two strands of the target sequence of both pAURHYG(ins)GFP and pAURHYG(rep)GFP. These experiments, presented in Tables 7 and 8, indicate that an oligonucleotide, HygE3T/74α, with sequence complementary to the sense strand (i.e. the strand of the target sequence that is identical to the mRNA) of the target sequence facilitates gene correction approximately ten-fold more efficiently than an oligonucleotide, HygE3T/74, with sequence complementary to the non-transcribed strand which serves as the template for the synthesis of RNA. As indicated in Table 7, this effect was observed over a range of oligonucleotide concentrations from 0-3.6 μg, although we did observe some variability in the difference between the two oligonucleotides (indicated in Table 7 as a fold difference between HygE3T/74α and HygE3T/74).

Furthermore, as shown in Table 8, we observe increased efficiency of correction by HygE3T/74α relative to HygE3T/74 regardless of whether the oligonucleotides were used to correct the base substitution mutation in pAURHYG(rep)GFP or the insertion mutation in pAURHYG(ins)GFP. The data presented in Table 8 further indicate that the single-stranded oligonucleotides correct a base substitution mutation more efficiently than an insertion mutation. However, this last effect was much less pronounced and the oligonucleotides of the invention are clearly able efficiently to correct both types of mutations in yeast cells. In addition, the role of transcription is investigated using plasmids with inducible promoters such as that described in Figure 10.

Optimization of oligonucleotide concentration. To determine the optimal concentration of oligonucleotide for the purpose of gene alteration, we test the ability of increasing concentrations of Hyg3T/74α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678. We chose this assay system because our previous experiments indicated that it supports the highest level of correction. However, this same approach could be used to determine the optimal concentration of any given oligonucleotide. We test the ability of Hyg3T/74α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678 over a range of oligonucleotide concentrations from 0-10.0 μg. As shown in Table 9, we observe that the correction efficiency initially increases with increasing oligonucleotide concentration, but then declines at the highest concentration tested.

Tables are attached hereto.

Table 6

Correction of an insertion mutation in pAURHYG(ins)GFP by HygGG/Rev, HygE3T/25 and HygE3T/74

Oligonucleotide Tested	Colonies on Hygromycin	Colonies on Aureobasidin (/10^5)	Correction Efficiency
HygGG/Rev	3	157	0.02
HygE3T/25	64	147	0.44
HygE3T/74	280	174	1.61
Kan70T	0	—	—

Table 7

An oligonucleotide targeting the sense strand of the target sequence corrects more efficiently.

Amount of Oligonucleotide (μg)	Colonies per hygromycin plate	
	HygE3T/74	HygE3T/74α
0	0	0
0.6	24	128 (8.4x)*
1.2	69	140 (7.5x)*
2.4	62	167 (3.8x)*
3.6	29	367 (15x)*

* The numbers in parentheses represent the fold increase in efficiency for targeting the non-transcribed strand as compared to the other strand of a DNA duplex that encodes a protein.

Table 8

Correction of a base substitution mutation is more efficient than correction of a frame shift mutation.

Oligonucleotide Tested (5 μg)	Plasmid tested (contained in LSY678)	
	pAURHYG(ins)GFP	pAURHYG(rep)GFP
HygE3T/74	72	277
HygE3T/74α	1464	2248
Kan70T	0	0

Table 9

Optimization of oligonucleotide concentration in electroporated yeast cells.

Amount (μg)	Colonies on hygromycin	Colonies on aureobasidin (/10^5)	Correction efficiency
0	0	67	0
1.0	5	64	0.08
2.5	47	30	1.57
5.0	199	33	6.08
7.5	383	39	9.79
10.0	191	33	5.79

Example 3
Cultured Cell Manipulation

Although disclosure in this example is directed to use of stem cells or human blood cells and microinjection, the microinjection procedures may also be used with cultured plant cells or protoplasts using any plant species, including those disclosed herein. Mononuclear cells are isolated from human umbilical cord blood of normal donors using Ficoll Hypaque (Pharmacia Biotech, Uppsala, Sweden) density centrifugation. CD34+ cells are immunomagnetically purified from mononuclear cells using either

the progenitor or Multisort Kits (Miltenyi Biotec, Auburn, CA). Lin^-CD38^- cells are purified from the mononuclear cells using negative selection with StemSep system according to the manufacturer's protocol (Stem Cell Technologies, Vancouver, CA). Cells used for microinjection are either freshly isolated or cryopreserved and cultured in Stem Medium (S Medium) for 2 to 5 days prior to microinjection. S Medium contains Iscoves' Modified Dulbecco's Medium without phenol red (IMDM) with 100 μg/ml glutamine/penicillin/streptomycin, 50 mg/ml bovine serum albumin, 50 μg/ml bovine pancreatic insulin, 1 mg/ml human transferrin, and IMDM; Stem Cell Technologies), 40 μg/ml low-density lipoprotein (LDL; Sigma, St. Louis, MO), 50 mM HEPEs buffer and 50 μM 2-mercaptoethanol, 20 ng/ml each of thrombopoietin, flt-3 ligand, stem cell factor and human IL-6 (Pepro Tech Inc., Rocky Hill, NJ). After microinjection, cells are detached and transferred in bulk into wells of 48 well plates for culturing.

35 mm dishes are coated overnight at 4° C with 50 μg/ml Fibronectin (FN) fragment CH-296 (Retronectin; TaKaRa Biomedicals, Panvera, Madison, WI) in phosphate buffered saline and washed with IMDM containing glutamine/penicillin/streptomycin. 300 to 2000 cells are added to cloning rings and attached to the plates for 45 minutes at 37° C prior to microinjection. After incubation, cloning rings are removed and 2 ml of S Medium are added to each dish for microinjection. Pulled injection needles with a range of 0.22 μm to 0.3 μm outer tip diameter are used. Cells are visualized with a microscope equipped with a temperature controlled stage set at 37° C and injected using an electronically interfaced Eppendorf Micromanipulator and Transjector. Successfully injected cells are intact, alive and remain attached to the plate post injection. Molecules that are flourescently labeled allow determination of the amount of oligonucleotide delivered to the cells.

For *in vitro* erythropoiesis from Lin^-CD38^- cells, the procedure of Malik, 1998 can be used. Cells are cultured in ME Medium for 4 days and then cultured in E Medium for 3 weeks. Erythropoiesis is evident by glycophorin A expression as well as the presence of red color representing the presence of hemoglobin in the cultured cells. The injected cells are able to retain their proliferative capacity and the ability to generate myeloid and erythoid progeny. CD34+ cells can convert a normal A (β^A) to sickle T (β^S) mutation in the β-globin gene or can be altered using any of the oligonucleotides of the invention herein for correction or alteration of a normal gene to a mutant gene. Alternatively, stem cells can be isolated from blood of humans having genetic disease mutations and the oligonucleotides of the invention can be used to correct a defect or to modify genomes within those cells.

Alternatively, non-stem cell populations of cultured cells can be manipulated using any method known to those of skill in the art including, for example, the use of polycations, cationic lipids,

liposomes, polyethylenimine (PEI), electroporation, biolistics, calcium phosphate precipitation, or any other method known in the art.

Biolistic delivery of oligonucleotide into plant cells may be accomplished according to the following method. One milliliter of packed cell volume of plant cell suspensions are subcultured onto plates containing solid medium [with Murashige and Skoog salts from Gibco/BRL, 500 mg/liter Mes, 1 mg/liter thiamin, 100 mg/liter myo-inositol, 180 mg/liter KH2PO4, 2.21 mg/liter 2,4-dichlorophenoxyacetic acid (2,4-D), and 30 g/liter sucrose (pH 5.7) and having 8 g/liter agar-agar from Sigma added before autoclaving]. By using a helium-driven particle gun such as that from BioRad and following manufacturers directions, oligonucleotides may be introduced to cells after precipitation onto 1 micrometer or comparable gold microcarriers (Bio-Rad). To precipitate onto microcarriers, 35 microliters of a particle suspension (60 mg of microcarriers per ml of 100% ethanol) is transferred to a 1.5 ml microcentrifuge tube, which is agitated on a vortex mixer. Then 40 microliter of resuspended oligonucleotide (60 ng/microliter water) is added; then 75 microliter of ice-cold 2.5 M CaCl2 is added; then 75 microliter of ice-cold 0.1 M spermidine is added. The tube is mixed vigorously or a vortex mixer for 10 min at room temperature. The particles are allowed to settle for 10 min and are centrifuged at 11,750 g for 30 sec. The supernatant is removed and the particles are resuspended in 50 microliter of 100% ethanol. An aliquot of 10 microliter of the resuspended particles are applied to each macro-projectile which is used to bombard each plate once at 900 psi (1 psi = 6.89 kPa) with a gap distance (distance from power source to macroprojectile) of 1 cm and a target distance (distance from microprojectile launch site to target material) of 10 cm.

An alternative method of delivery can be used as follows. Cultured cells are suspended in liquid N6 medium and then plated on a VWR Scientific glass fiber filter. About 0.4 microgram of oligonucleotide are precipitated with 15 microliter of 2.5 mM CaCl2 and 5 microliter of 0.1 M spermidine onto 25 microgram of 1.0 micrometer gold particles. Microprojectile bombardment is performed by using a Bio-Rad PDS-1000 He particle delivery system or comparable machine following manufacturers instructions. Alterations in oligonucleotide concentrations can be employed to determine the optimum concentration of oligonucleotide according to the procedures described herein for any particular oligonucleotide of the invention.

Alternatively, the oligonucleotide of the invention may be delivered to a plant cell by electroporation of a protoplast derived from a plant part. The protoplasts may be formed by enzymatic treatment of a plant part, particularly a leaf, according to techniques such as those in Gallois et al., Methods in Molecular Biology 55: 89-107 by Humana Press. Such conditions for electroporation use

about 3×10^5 protoplasts in a total volume of about 0.3 ml with a concentration of oligonucleotide of between 0.6 to 4 microgram per ml.

EXAMPLE 4

Plant Cells

The oligonucleotides of the invention can also be used to repair or direct a mutagenic event in plants and animal cells. Although little information is available on plant mutations amongst natural cultivars, the oligonucleotides of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying Gln can be modified at a specific site to TAA; a AAG codon specifying Lys can be modified to UAG at a specific site; and a CGA codon for Arg can be modified to a UGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a defective truncated protein, shortened at the site of the stop codon

. Alternatively, frameshift additions or deletions can be directed into the genome at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

For introduction of a T-DNA, including the T-DNA in the plasmid of Figure 11, into a plant cell, *Agrobacterium tumefaciens* is used. These techniques are routine standard techniques known in the art. For example, one method follows. We transform *A. tumefaciens* is transformed by electroporation (using a BioRad Gene Pulser™). Competent *A. tumefaciens* is prepared using a method similar to that of preparing competent *E. coli* by suspending a freshly grown culture three times in ice-cold water and a final resuspension in 10% glycerol. Electroporation conditions are a 0.2 cm gap cuvette at a setting of 25 μF, 200 Ω and 2.5 kV.

A. tumefaciens containing a plasmid with a T-DNA is then used to introduce the T-DNA into a plant cell using routine standard techniques known in the art. For example, we transform Arabidopsis by vacuum infiltration or by dipping flowers in an Agrobacterium solution containing a surfactant, e.g. L-77. Seeds are then collected, grown and screened for presence of the T-DNA. Alternatively, Agrobacterium can be used to transform callus tissue and the callus tissue can then be used to regenerate transformed plants.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some

detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Notes on the tables presented below:

Each of the following tables presents, for the specified gene, a plurality of mutations that are known to confer a relevant phenotype and, for each mutation, the oligonucleotides that can be used to correct the respective mutation site-specifically in the genome according to the present invention.

The left-most column identifies each alteration or mutation and the phenotype that the alteration/mutation confers.

For most entries, the mutation/alteration is identified at both the nucleic acid and protein level. At the amino acid level, mutations are presented according to the following standard nomenclature. The centered number identifies the position of the mutated codon in the protein sequence; to the left of the number is the wild type residue and to the right of the number is the mutant codon. Terminator codons are shown as "TERM". At the nucleic acid level, the entire triplet of the wild type and mutated codons is shown.

The middle column presents, for each mutation, four oligonucleotides capable of repairing the mutation site-specifically in the genome or in cloned DNA including DNA in artificial chromosomes, episomes, plasmids, or other types of vectors. The oligonucleotides of the invention, however, may include any of the oligonucleotides sharing portions of the sequence of the 121 base sequence. Thus, oligonucleotides of the invention for each of the depicted targets may be 18, 19, 20 up to about 121 nucleotides in length. Sequence may be added non-symmetrically.

All oligonucleotides are presented, per convention, in the 5' to 3' orientation. The nucleotide that effects the change in the genome is underlined and presented in bold.

The first of the four oligonucleotides for each mutation is a 121 nt oligonucleotide centered about the repair/altering nucleotide. The second oligonucleotide, its reverse complement, targets the opposite strand of the DNA duplex for repair/alteration. The third oligonucleotide is the minimal 17 nt domain of the first oligonucleotide, also centered about the repair/alteration nucleotide. The fourth oligonucleotide is the reverse complement of the third, and thus represents the minimal 17 nt domain of the second.

The third column of each table presents the SEQ ID NO: of the respective repair oligonucleotide.

Example 5

Engineering herbicide resistant plants

Chemical weed control is an important tool of modern agriculture and many herbicides have been developed for this purpose. Their use has resulted in substantial increases in the yields of many crops, including, for example, maize, soybeans, and cotton. Thus while the use of fertilizers and new high-yielding crop varieties have contributed greatly to the "green revolution," chemical weed control has also been at the forefront of technological achievement.

Herbicides having broad-spectrum activity are particularly useful because they obviate the need for multiple herbicides targeting different classes of weeds. The problem with such herbicides is that they typically also affect crops which are exposed to the herbicide. One way to overcome this is to generate plants which are resistant to one or more broad-spectrum herbicides. Such herbicide-tolerant plants may reduce the need for tillage to control weeds, thereby effectively reducing soil erosion and can reduce the quantity and number of different herbicides applied in the field.

Common herbicides used, for example, include those that inhibit the enzyme 5-enolpyruvyl-3-phosphoshikimic acid synthase (EPSPS), for example N-phosphonomethyl-glycine (e.g. glyphosate), those that inhibit acetolactate synthase (ALS) activity, for example the sulfonylureas and related herbicides, and those that inhibit dihydropteroate synthase, for example methyl[(4-amino-phenyl)sulfonyl]carbamate (e.g. Asulam). Herbicide-tolerant plants can be produced by several methods, including, for example, introducing into the genome of the plant the ability to degrade the herbicide, the capacity to produce a higher level of the targeted enzyme, and/or expressing an herbicide-tolerant allele of the enzyme.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes that confer herbicide resistance.

Table 10
Genome-Altering Oligos Conferring Glyphosate Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Glyphosate Resistance EPSPS *Arabidopsis thaliana* Gly97Ala GGC-GCC	AAGCGTCGGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTCTTATTAAGCTTCCTG**C**CTCCAAGTCTCTATCAAATCGGATCCTGCTTCTCGCTGCTCTGTCTGAGGTATATATCAC	4341
	GTGATATATACCTCAGACAGAGCAGCGAGAAGCAGGATCCGATTTGATAGAGACTTGGAG**G**CAGGAAGCTTAATAAGACCGGAGATTTCTCTAATGGGTTGAAGTACAATCTCCGACGCTT	4342
	GCTTCCTG**C**CTCCAAGT	4343
	ACTTGGAG**G**CAGGAAGC	4344
Glyphosate Resistance EPSPS *Brassica napus* Gly93Ala GGA-GCA	AAGCTTCAGAGATTGTGCTTCAACCAATCAGAGAAATCTCGGGTCTCATTAAGCTACCCG**C**ATCCAAATCTCTCTCCAATCGGATCCTCCTTCTTGCCGCTCTATCTGAGGTACATATACT	4345
	AGTATATGTACCTCAGATAGAGCGGCAAGAAGGAGGATCCGATTGGAGAGAGATTTGGAT**G**CGGGTAGCTTAATGAGACCCGAGATTTCTCTGATTGGTTGAAGCACAATCTCTGAAGCTT	4346
	GCTACCCG**C**ATCCAAAT	4347
	ATTTGGAT**G**CGGGTAGC	4348
Glyphosate Resistance EPSPS 1 *Nicotiana tabacum* Gly95Ala GGT-GCT	AGCCCAACGAGATTGTGCTGCAACCCATCAAAGATATATCAGGCACTGTTAAATTGCCTG**C**TTCTAAATCCCTTTCCAATCGTATTCTCCTTCTTGCTGCCCTTTCTAAGGGAAGGACTGT	4349
	ACAGTCCTTCCCTTAGAAAGGGCAGCAAGAAGGAGAATACGATTGGAAAGGGATTTAGAA**G**CAGGCAATTTAACAGTGCCTGATATATCTTTGATGGGTTGCAGCACAATCTCGTTGGGCT	4350
	ATTGCCTG**C**TTCTAAAT	4351
	ATTTAGAA**G**CAGGCAAT	4352
Glyphosate Resistance EPSPS 2 *Nicotiana tabacum* Gly62Ala GGA-GCA	ATTGTTTCCTTGGTACGAAATGTCCTCCTGTTCGAATTGTCAGCAAGGGAGGCCTTCCCG**C**AGGGAAGGTAAAGCTCTCTGGATCAATTAGCAGCCAGTACTTGACTGCTCTGCTTATGGC	4353
	GCCATAAGCAGAGCAGTCAAGTACTGGCTGCTAATTGATCCAGAGAGCTTTACCTTCCCT**G**CGGGAAGGCCTCCCTTGCTGACAATTCGAACAGGAGGACATTTCGTACCAAGGAAACAAT	4354
	CCTTCCCG**C**AGGGAAGG	4355
	CCTTCCCT**G**CGGGAAGG	4356
Glyphosate Resistance EPSPS *Zea mays* Gly168Ala GGT-GCT	ATTGTTTCCTTGGCACTGACTGCCCACCTGTTCGTGTCAATGGAATCGGAGGGCTACCTG**C**TGGCAAGGTCAAGCTGTCTGGCTCCATCAGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	4357
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAGCCAGACAGCTTGACCTTGCCA**G**CAGGTAGCCCTCCGATTCCATTGACACGAACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	4358

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCTACCTG**C**TGGCAAGG	4359
	CCTTGCCA**G**CAGGTAGC	4360
Glyphosate Resistance EPSPS *Oryza sativa* Gly115Ala GGT-GCT	ACTGTTTCCTTGGCACTGAATGCCCACCTGTTCGTGTCAAGGGAATTGGAGGACTTCCTG**C**TGGCAAGGTTAAGCTCTCTGGTTCCATCAGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	4361
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAACCAGAGAGCTTAACCTTGCCA**G**CAGGAAGTCCTCCAATTCCCTTGACACGAACAGGTGGGCATTCAGTGCCAAGGAAACAGT	4362
	ACTTCCTG**C**TGGCAAGG	4363
	CCTTGCCA**G**CAGGAAGT	4364
Glyphosate Resistance EPSPS *Petunia x hybrida* Gly93Ala GGC-GCC	AGCCTTCTGAGATAGTGTTGCAACCCATTAAAGAGATTTCAGGCACTGTTAAATTGCCTG**C**CTCTAAATCATTATCTAATAGAATTCTCCTTCTTGCTGCCTTATCTGAAGGAACAACTGT	4365
	ACAGTTGTTCCTTCAGATAAGGCAGCAAGAAGGAGAATTCTATTAGATAATGATTTAGAG**G**CAGGCAATTTAACAGTGCCTGAAATCTCTTTAATGGGTTGCAACACTATCTCAGAAGGCT	4366
	ATTGCCTG**C**CTCTAAAT	4367
	ATTTAGAG**G**CAGGCAAT	4368
Glyphosate Resistance EPSPS *Lycopersicon esculentum* Gly97Ala GGT-GCT	AACCCCATGAGATTGTGCTAGNACCCATCAAAGATATATCTGGTACTGTTAAATTACCCG**C**TTCGAAATCCCTTTCCAATCGTATTCTCCTTCTTGCTGCCCTTTCTGAGGGAAGGACTGT	4369
	ACAGTCCTTCCCTCAGAAAGGGCAGCAAGAAGGAGAATACGATTGGAAAGGGATTTCGAA**G**CGGGTAATTTAACAGTACCAGATATATCTTTGATGGGTNCTAGCACAATCTCATGGGGTT	4370
	ATTACCCG**C**TTCGAAAT	4371
	ATTTCGAA**G**CGGGTAAT	4372
Glyphosate Resistance EPSPS *Lolium rigidum* Gly107Ala GGT-GCT	ATTGTTTCCTTGGCACTGACTGCCCACCTGTTCGKATCAACGGCATTGGAGGGCTACCTG**C**TGGCAAGGTTAAGCTGTCTGGTTCCATCAGCAGCCAATACTTGAGTTCCTTGCTGATGGC	4373
	GCCATCAGCAAGGAACTCAAGTATTGGCTGCTGATGGAACCAGACAGCTTAACCTTGCCA**G**CAGGTAGCCCTCCAATGCCGTTGATCGAACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	4374
	GCTACCTG**C**TGGCAAGG	4375
	CCTTGCCA**G**CAGGTAGC	4376

Table 11

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS *Arabidopsis thaliana* Pro197Ser CCT-TCT	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCA ATCACAGGACAAGTC**T**CTCGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4377
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGAG**A**GACTTGTCCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	4378
	GACAAGTC**T**CTCGTCGT	4379
	ACGACGAG**A**GACTTGTC	4380
Sulfonylurea Resistance ALS *Arabidopsis thaliana* Pro197Gln CCT-CAG	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCA ATCACAGGACAAGTCC**AG**CGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4381
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACG**CT**GGACTTGTCCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	4382
	ACAAGTCC**AG**CGTCGTC	4383
	TACGACG**CT**GGACTTGT	4384
Sulfonylurea Resistance ALS *Arabidopsis thaliana* Pro197Gln CCT-CAA	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCA ATCACAGGACAAGTCC**AA**CGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4385
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACG**TT**GGACTTGTCCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	4386
	ACAAGTCC**AA**CGTCGTA	4387
	TACGACG**TT**GGACTTGT	4388
Imidazolinone Resistance ALS *Arabidopsis thaliana* Ser653Asn AGT-AAC	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGA**AC**GGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4389
	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACC**GT**TCGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	4390
	GATCCCGA**AC**GGTGGCA	4391
	TGCCACC**GT**TCGGGATC	4392

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Imidazolinone Resistance ALS *Arabidopsis thaliana* Ser653Asn AGT-AAT	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGA**AT**GGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4393
	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACC**AT**TCGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	4394
	GATCCCGA**AT**GGTGGCA	4395
	TGCCACC**AT**TCGGGATC	4396
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCG CCATCACGGGCCAGGTC**T**CCCGCCGCATGATCGGCACCGACGC CTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	4397
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGG**A**GACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	4398
	GCCAGGTC**T**CCCGCCGC	4399
	GCGGCGGG**A**GACCTGGC	4400
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAA	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCC**AA**CGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4401
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCG**TT**GGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4402
	CCAGGTCC**AA**CGCCGCA	4403
	TGCGGCG**TT**GGACCTGG	4404
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAG	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCC**AG**CGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4405
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCG**CT**GGACCTGGCCCGTGATGGCGACCATC GGGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4406
	CCAGGTCC**AG**CGCCGCA	4407
	TGCGGCG**CT**GGACCTGG	4408
Imidazolinone Resistance ALS *Oryza sativa* Ile627Asn ATT-AAT	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCCTATGATCCCAA**A**TGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4409
	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCA**T**TTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC	4410
	GATCCCAA**A**TGGGGGCG	4411

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCCCCCATTTGGGATC	4412
Sulfonylurea Resistance ALS *Zea mays* Pro165Ser CCG-TCG	TCCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGCCATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCCTTCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4413
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGGTGCCAATCATGCGTCGCGACACCTGTCCCGTGATGGCGACCATGGGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	4414
	GACAGGTGTCGCGACGC	4415
	GCGTCGCGACACCTGTC	4416
Sulfonylurea Resistance ALS *Zea mays* Pro165Gln CCG-CAG	CCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGCCATCACGGGACAGGTGCAGCGACGCATGATTGGCACCGACGCCTTCCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4417
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGGTGCCAATCATGCGTCGCTGCACCTGTCCCGTGATGGCGACCATGGGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGG	4418
	ACAGGTGCAGCGACGCA	4419
	TGCGTCGCTGCACCTGT	4420
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAT	GGCCGTACCTCTTGGATATAATCGTCCCACACCAGGAGCATGTGTTGCCTATGATCCCTAATGGTGGGGCTTTCAAGGATATGATCCTGGATGGTGATGGCAGGACTGTGTACTGATCTAA	4421
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCTTGAAAGCCCCACCATTAGGGATCATAGGCAACACATGCTCCTGGTGTGGGACGATTATATCCAAGAGGTACGGCC	4422
	GATCCCTAATGGTGGGG	4423
	CCCCACCATTAGGGATC	4424
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAC	GGCCGTACCTCTTGGATATAATCGTCCCACACCAGGAGCATGTGTTGCCTATGATCCCTAACGGTGGGGCTTTCAAGGATATGATCCTGGATGGTGATGGCAGGACTGTGTACTGATCTAA	4425
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCTTGAAAGCCCCACCGTTAGGGATCATAGGCAACACATGCTCCTGGTGTGGGACGATTATATCCAAGAGGTACGGCC	4426
	GATCCCTAACGGTGGGG	4427
	CCCCACCGTTAGGGATC	4428
Sulfonylurea Resistance ALS *Lolium multiflorum* Pro167Ser CCG-TCG	TCCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGCCATCACGGGGCAGGTCTCGCGCCGCATGATCGGCACGGACGCCTTCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4429
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGTGCCGATCATGCGGCGCGAGACCTGCCCCGTGATGGCCACCATGGGGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGGA	4430

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGCAGGTCTCGCGCCGC	4431
	GCGGCGCGAGACCTGCC	4432
Sulfonylurea Resistance ALS *Lolium multiflorum* Pro167Gln CCG-CAG	CCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGCCATCACGGGGCAGGTCCAGCGCCGCATGATCGGCACGGACGCCTTCCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4433
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGTGCCGATCATGCGGCGCTGGACCTGCCCCGTGATGGCCACCATGGGGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGG	4434
	GCAGGTCCAGCGCCGCA	4435
	TGCGGCGCTGGACCTGC	4436
Imidazolinone Resistance ALS *Lolium multiflorum* Ser623Asn AGC-AAC	CTGGGCCATACTTGTTGGATATCATCGTCCCTCACCAGGAGCATGTGCTGCCTATGATCCCTAACGGTGGTGCTTTCAAGGACATTATCATGGAAGGTGATGGCAGGATTTCGTATTAAAC	4437
	GTTTAATACGAAATCCTGCCATCACCTTCCATGATAATGTCCTTGAAAGCACCACCGTTAGGGATCATAGGCAGCACATGCTCCTGGTGAGGGACGATGATATCCAACAAGTATGGCCCAG	4438
	GATCCCTAACGGTGGTG	4439
	CACCACCGTTAGGGATC	4440
Sulfonylurea Resistance ALS *Hordeum vulgare* Pro68Ser CCA-TCA	TCCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGCCATCACGGGCCAGGTCTCACGCCGCATGATCGGCACGGACGCGTTCCAGGAGACGCCCATAGTGGAGGTCACGCGCT	4441
	AGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGTGCCGATCATGCGGCGTGAGACCTGGCCCGTGATGGCGACCATGGGGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGGA	4442
	GCCAGGTCTCACGCCGC	4443
	GCGGCGTGAGACCTGGC	4444
Sulfonylurea Resistance ALS *Hordeum vulgare* Pro68Gln CCA-CAA	CCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGCCATCACGGGCCAGGTCCAACGCCGCATGATCGGCACGGACGCGTTCCAGGAGACGCCCATAGTGGAGGTCACGCGCTC	4445
	GAGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGTGCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATGGGGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGG	4446
	CCAGGTCCAACGCCGCA	4447
	TGCGGCGTTGGACCTGG	4448

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Imidazolinone Resistance ALS *Hordeum vulgare* Ser524Asn AGC-AAC	CCCAGGGCCGTACCTGCTGGATATCATTGTCCCGCATCAGGAGC ACGTGCTGCCTATGATCCCAA**A**CGGTGGTGCTTTCAAGGACATGA TCATGGAGGGTGATGGCAGGACCTCGTACTGA	4449
	TCAGTACGAGGTCCTGCCATCACCCTCCATGATCATGTCCTTGAA AGCACCACCG**T**TTGGGATCATAGGCAGCACGTGCTCCTGATGCG GGACAATGATATCCAGCAGGTACGGCCCTGGG	4450
	GATCCCAA**A**CGGTGGTG	4451
	CACCACCG**T**TTGGGATC	4452
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTC**T**CTCGTCGGATGATCGGTACCGATGCTTTC CAGGAAACTCCAATTGTTGAGGTAACAAGGT	4453
	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC CGATCATCCGACGAG**A**GACTTGACCAGTGATCGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT	4454
	GTCAAGTC**T**CTCGTCGG	4455
	CCGACGAG**A**GACTTGAC	4456
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCC**AA**CGTCGGATGATCGGTACCGATGCTTTCC AGGAAACTCCAATTGTTGAGGTAACAAGGTC	4457
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACG**TT**GGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4458
	TCAAGTCC**AA**CGTCGGA	4459
	TCCGACG**TT**GGACTTGA	4460
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCC**AG**CGTCGGATGATCGGTACCGATGCTTTCC AGGAAACTCCAATTGTTGAGGTAACAAGGTC	4461
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACG**CT**GGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4462
	TCAAGTCC**AG**CGTCGGA	4463
	TCCGACG**CT**GGACTTGA	4464
Imidazolinone Resistance ALS *Gossypium hirsutum* Ser642Asn AGT-AAT	GACCTTACTTGTTGGATGTGATTGTCCCACATCAAGAACATGTCCT GCCTATGATCCCCA**A**TGGAGGCGCTTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	4465
	TGAGGTCAATATTGTGTTCTTCCATCACCCTCTGTGATCACATCTT TGAAAGCGCCTCCA**T**TGGGGATCATAGGCAGGACATGTTCTTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	4466
	GATCCCCA**A**TGGAGGCG	4467

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCCTCCATTGGGGATC	4468
Sulfonylurea Resistance ALS *Amaranthus retroflexus* Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCATTACTGGGCAAGTTTCCCGGCGTATGATTGGTACTGATGCTTTTCAAGAGACTCCAATTGTTGAGGTAACTCGAT	4469
	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACCAATCATACGCCGGGAAACTTGCCCAGTAATGGCGACAAGAGGGACTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4470
	GGCAAGTTTCCCGGCGT	4471
	ACGCCGGGAAACTTGCC	4472
Sulfonylurea Resistance ALS *Amaranthus retroflexus* Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCATTACTGGGCAAGTTCAACGGCGTATGATTGGTACTGATGCTTTTCAAGAGACTCCAATTGTTGAGGTAACTCGATC	4473
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACCAATCATACGCCGTTGAACTTGCCCAGTAATGGCGACAAGAGGGACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4474
	GCAAGTTCAACGGCGTA	4475
	TACGCCGTTGAACTTGC	4476
Sulfonylurea Resistance ALS *Amaranthus retroflexus* Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCATTACTGGGCAAGTTCAGCGGCGTATGATTGGTACTGATGCTTTTCAAGAGACTCCAATTGTTGAGGTAACTCGATC	4477
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACCAATCATACGCCGCTGAACTTGCCCAGTAATGGCGACAAGAGGGACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4478
	GCAAGTTCAGCGGCGTA	4479
	TACGCCGCTGAACTTGC	4480
Imidazolinone Resistance ALS *Amaranthus retroflexus* Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGCTGCCTATGATCCCTAACGGTGCCGCCTTCAAGGACACCATAACAGAGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4481
	ACCAACTAATAAGCCCTTCTTCCATCACCCTCTGTTATGGTGTCCTTGAAGGCGGCACCGTTAGGGATCATAGGCAGCACATGCTCCTGATGTGGTACGATTACATCCAGCAGATACGGTC	4482
	GATCCCTAACGGTGCCG	4483
	CGGCACCGTTAGGGATC	4484

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS 1 *Nicotiana tabacum* Pro194Ser CCA-TCA	AGCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGC TATAACAGGTCAAGTGTCACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAACTAGAT	4485
	ATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTACC TATCATCCTACGTGACACTTGACCTGTTATAGCAACAATGGGGAC GCTATCCAGTAGCGCGTCAGCGAGGCCGCT	4486
	GTCAAGTGTCACGTAGG	4487
	CCTACGTGACACTTGAC	4488
Sulfonylurea Resistance ALS 1 *Nicotiana tabacum* Pro194Gln CCA-CAA	GCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGCT ATAACAGGTCAAGTGCAACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAACTAGATC	4489
	GATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTAC CTATCATCCTACGTTGCACTTGACCTGTTATAGCAACAATGGGGA CGCTATCCAGTAGCGCGTCAGCGAGGCCGC	4490
	TCAAGTGCAACGTAGGA	4491
	TCCTACGTTGCACTTGA	4492
Imidazolinone Resistance ALS 1 *Nicotiana tabacum* Ser650Asn AGT-AAT	GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTTT ACCTATGATTCCCAATGGCGGAGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAGTTCCTATTGAGTTTG	4493
	CAAACTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCTCCGCCATTGGGAATCATAGGTAAAACATGTTCCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4494
	GATTCCCAATGGCGGAG	4495
	CTCCGCCATTGGGAATC	4496
Sulfonylurea Resistance ALS 2 *Nicotiana tabacum* Pro191Ser CCA-TCA	AGTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGC TATAACCGGTCAAGTGTCACGTAGGATGATCGGTACTGATGCTTTT CAGGAAACTCCGATTGTTGAGGTAACTAGAT	4497
	ATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTACC GATCATCCTACGTGACACTTGACCGGTTATAGCAACAATGGGGAC GCTATCCAGTAGGGCGTCCGCGAGGCCACT	4498
	GTCAAGTGTCACGTAGG	4499
	CCTACGTGACACTTGAC	4500
Sulfonylurea Resistance ALS 2 *Nicotiana tabacum* Pro191Gln CCA-CAA	GTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGCT ATAACCGGTCAAGTGCAACGTAGGATGATCGGTACTGATGCTTTT CAGGAAACTCCGATTGTTGAGGTAACTAGATC	4501
	GATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTAC CGATCATCCTACGTTGCACTTGACCGGTTATAGCAACAATGGGGA CGCTATCCAGTAGGGCGTCCGCGAGGCCAC	4502
	TCAAGTGCAACGTAGGA	4503

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCTACGTTGCACTTGA	4504
Imidazolinone Resistance ALS 2 *Nicotiana tabacum* Ser647Asn AGT-AAT	GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTCTACCTATGATTCCCAATGGCGGGGCTTTCAAAGATGTGATCACAGAGGGTGACGGGAGAAGTTCCTATTGACTTTG	4505
	CAAAGTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTTTGAAAGCCCCGCCATTGGGAATCATAGGTAGAACATGTTCCTGATGAGGTACAATCACATCCAACAAGTATGGCC	4506
	GATTCCCAATGGCGGGG	4507
	CCCCGCCATTGGGAATC	4508
Sulfonylurea Resistance ALS *Xanthium* spp. Pro175Ser CCC-TCC	AGTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTATTACTGGTCAAGTTTCCAGGAGAATGATTGGAACAGATGCGTTTCAAGAAACCCCTATTGTTGAGGTAACACGTT	4509
	AACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCCAATCATTCTCCTGGAAACTTGACCAGTAATAGCAACCATTGGAACACTGTCTAATAAAGCATCAGCAAGACCACT	4510
	GTCAAGTTTCCAGGAGA	4511
	TCTCCTGGAAACTTGAC	4512
Sulfonylurea Resistance ALS *Xanthium* spp. Pro175Gln CCC-CAA	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTATTACTGGTCAAGTTCAAAGGAGAATGATTGGAACAGATGCGTTTCAAGAAACCCCTATTGTTGAGGTAACACGTTC	4513
	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCCAATCATTCTCCTTTGAACTTGACCAGTAATAGCAACCATTGGAACACTGTCTAATAAAGCATCAGCAAGACCAC	4514
	TCAAGTTCAAAGGAGAA	4515
	TTCTCCTTTGAACTTGA	4516
Sulfonylurea Resistance ALS *Xanthium* spp. Pro175Gln CCC-CAG	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTATTACTGGTCAAGTTCAGAGGAGAATGATTGGAACAGATGCGTTTCAAGAAACCCCTATTGTTGAGGTAACACGTTC	4517
	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCCAATCATTCTCCTCTGAACTTGACCAGTAATAGCAACCATTGGAACACTGTCTAATAAAGCATCAGCAAGACCAC	4518
	TCAAGTTCAGAGGAGAA	4519
	TTCTCCTCTGAACTTGA	4520
Imidazolinone Resistance ALS *Xanthium* spp. Ala631Asn GCT-AAT	GGGCCTTACTTGTTGGATGTGATCGTGCCCCATCAAGAACATGTGTTGCCCATGATCCCGAATGGTGGAGGTTTCATGGATGTGATCACCGAAGGCGACGGCAGAATGAAATATTGAGCTT	4521
	AAGCTCAATATTTCATTCTGCCGTCGCCTTCGGTGATCACATCCATGAAACCTCCACCATTCGGGATCATGGGCAACACATGTTCTTGATGGGGCACGATCACATCCAACAAGTAAGGCCC	4522

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATCCCG**AA**TGGTGGA	4523
	TCCACCA**TT**CGGGATCA	4524
Sulfonylurea Resistance ALS *Bassia scoparia* Pro189Ser CCG-TCG	TCCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCG ATCACGGGGCAGGTG**T**CGCGGCGAATGATTGGGACGGATGCTTT TCAGGAGACTCCTATTGTTGAGGTAACACGGT	4525
	ACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTCC CAATCATTCGCCGCG**A**CACCTGCCCCGTGATCGCCACCAGTGGA ACGGAATCGAGCAAAGCATCAGCAAACCCGGA	4526
	GGCAGGTG**T**CGCGGCGA	4527
	TCGCCGCG**A**CACCTGCC	4528
Sulfonylurea Resistance ALS *Bassia scoparia* Pro189Gln CCG-CAG	CCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCGA TCACGGGGCAGGTGC**A**GCGGCGAATGATTGGGACGGATGCTTTT CAGGAGACTCCTATTGTTGAGGTAACACGGTC	4529
	GACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTC CCAATCATTCGCCGC**T**GCACCTGCCCCGTGATCGCCACCAGTGG AACGGAATCGAGCAAAGCATCAGCAAACCCGG	4530
	GCAGGTGC**A**GCGGCGAA	4531
	TTCGCCGC**T**GCACCTGC	4532
Imidazolinone Resistance ALS *Bassia scoparia* Ser649Asn AGT-AAT	GACCTTACCTGCTTGATGTGATTGTACCTCATCAGGAGCATGTGC TGCCTATGATTCCTA**A**TGGTGCAGCCTTCAAGGATATCATTAACGA AGGTGATGGAAGAACAAGTTATTGATGTTC	4533
	GAACATCAATAACTTGTTCTTCCATCACCTTCGTTAATGATATCCTT GAAGGCTGCACCA**T**TAGGAATCATAGGCAGCACATGCTCCTGATG AGGTACAATCACATCAAGCAGGTAAGGTC	4534
	GATTCCTA**A**TGGTGCAG	4535
	CTGCACCA**T**TAGGAATC	4536
Sulfonylurea Resistance ALS 1 *Brassica napus* Pro182Ser CCT-TCT	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGC CATTACAGGACAGGTC**T**CTCGCCGGATGATCGGTACTGACGCCTT CCAAGAGACACCAATCGTTGAGGTAACGAGGT	4537
	ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTAC CGATCATCCGGCGAG**A**GACCTGTCCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	4538
	GACAGGTC**T**CTCGCCGG	4539
	CCGGCGAG**A**GACCTGTC	4540

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS 1 *Brassica napus* Pro182Gln CCT-CAA	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCATTACAGGACAGGTCCAACGCCGGATGATCGGTACTGACGCCTTCCAAGAGACACCAATCGTTGAGGTAACGAGGTC	4541
	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACCGATCATCCGGCGTTGGACCTGTCCTGTAATGGCGACAAGAGGAACACTGTCAAGCATCGCGTCTGCTAACCCGC	4542
	ACAGGTCCAACGCCGGA	4543
	TCCGGCGTTGGACCTGT	4544
Sulfonylurea Resistance ALS 1 *Brassica napus* Pro182Gln CCT-CAG	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCATTACAGGACAGGTCCAGCGCCGGATGATCGGTACTGACGCCTTCCAAGAGACACCAATCGTTGAGGTAACGAGGTC	4545
	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACCGATCATCCGGCGCTGGACCTGTCCTGTAATGGCGACAAGAGGAACACTGTCAAGCATCGCGTCTGCTAACCCGC	4546
	ACAGGTCCAGCGCCGGA	4547
	TCCGGCGCTGGACCTGT	4548
Imidazolinone Resistance ALS 1 *Brassica napus* Ser638Asn AGT-AAT	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGTTACCGATGATCCCAAATGGTGGCACTTTCAAAGATGTAATAACAGAAGGGGATGGTCGCACTAAGTACTGAGAGAT	4549
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCTGTTATTACATCTTTGAAAGTGCCACCATTTGGGATCATCGGTAACACATGTTCTTGGTGCGGACATATCACATCCAACAGGTATGGTC	4550
	GATCCCAAATGGTGGCA	4551
	TGCCACCATTTGGGATC	4552
Sulfonylurea Resistance ALS 2 *Brassica napus* Pro126Ser CCC-TCC	CAGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCATTACAGGACAGGTTCCTCGCCGGATGATCGGTACTGACGCCTTCCAAGAGACACCAATCGTTGAGGTAACGAGG	4553
	CCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACCGATCATCCGGCGAGGAACCTGTCCTGTAATGGCGACAAGAGGAACACTGTCAAGCATCGCGTCTGCTAACCCGCTG	4554
	GGACAGGTTCCTCGCCG	4555
	CGGCGAGGAACCTGTCC	4556
Sulfonylurea Resistance ALS 2 *Brassica napus* Pro126Gln CCC-CAG	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCATTACAGGACAGGTCACTCGCCGGATGATCGGTACTGACGCCTTCCAAGAGACACCAATCGTTGAGGTAACGAGGT	4557
	ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACCGATCATCCGGCGAGTGACCTGTCCTGTAATGGCGACAAGAGGAACACTGTCAAGCATCGCGTCTGCTAACCCGCT	4558
	GACAGGTCACTCGCCGG	4559

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGGCGAGTGACCTGTC	4560
Imidazolinone Resistance ALS 2 *Brassica napus* Ser582Asn AGT-AAT	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT TACCGATGATCCCAAATGGTGGCACTTTCAAAGATGTAATAACAGA AGGGGATGGTCGCACTAAGTACTGAGAGAT	4561
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCTGTTATTACATCTT TGAAAGTGCCACCATTTGGGATCATCGGTAACACATGTTCTTGGT GCGGACATATCACATCCAACAGGTATGGTC	4562
	GATCCCAAATGGTGGCA	4563
	TGCCACCATTTGGGATC	4564
Sulfonylurea Resistance ALS 3 *Brassica napus* Pro179Ser CCT-TCT	AGCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGC CATCACAGGACAGGTCTCTCGCCGGATGATCGGTACTGACGCGT TCCAAGAGACGCCAATCGTTGAGGTAACGAGGT	4565
	ACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTAC CGATCATCCGGCGAGAGACCTGTCCTGTGATGGCGACGAGAGGA ACACTGTCAAGCATCGCGTCGGCTAACCCGCT	4566
	GACAGGTCTCTCGCCGG	4567
	CCGGCGAGAGACCTGTC	4568
Sulfonylurea Resistance ALS 3 *Brassica napus* Pro179Gln CCT-CAA	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGCC ATCACAGGACAGGTCCAACGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	4569
	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCGTTGGACCTGTCCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGTCGGCTAACCCGC	4570
	ACAGGTCCAACGCCGGA	4571
	TCCGGCGTTGGACCTGT	4572
Sulfonylurea Resistance ALS 3 *Brassica napus* Pro179Gln CCT-CAG	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGCC ATCACAGGACAGGTCCAGCGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	4573
	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCGCTGGACCTGTCCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGTCGGCTAACCCGC	4574
	ACAGGTCCAGCGCCGGA	4575
	TCCGGCGCTGGACCTGT	4576
Imidazolinone Resistance ALS 3 *Brassica napus* Ser635Asn AGT-AAT	GACCGTACCTGTTGGATGTCATCTGTCCGCACCAAGAACATGTGT TACCGATGATCCCAAATGGTGGCACTTTCAAAGATGTAATAACCG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	4577
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCGGTTATTACATCTT TGAAAGTGCCACCATTTGGGATCATCGGTAACACATGTTCTTGGT GCGGACAGATGACATCCAACAGGTACGGTC	4578

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GATCCCAAATGGTGGCA	4579
	TGCCACCATTTGGGATC	4580
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCG CCATCACGGGCCAGGTCTCCCGCCGCATGATCGGCACCGACGC CTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	4581
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGGAGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	4582
	GCCAGGTCTCCCGCCGC	4583
	GCGGCGGGAGACCTGGC	4584
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAA	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCCAACGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4585
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4586
	CCAGGTCCAACGCCGCA	4587
	TGCGGCGTTGGACCTGG	4588
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAG	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCCAGCGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4589
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGCTGGACCTGGCCCGTGATGGCGACCATC GGGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4590
	CCAGGTCCAGCGCCGCA	4591
	TGCGGCGCTGGACCTGG	4592
Imidazolinone Resistance ALS *Oryza sativa* Ser627Asn AGT-AAT	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCCTATGATCCCAAATGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4593
	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCATTTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC	4594
	GATCCCAAATGGGGGCG	4595
	CGCCCCCATTTGGGATC	4596

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS *Zea mays* Pro165Ser CCG-TCG	TCTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGCCATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCCTTTCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4597
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGTGCCAATCATGCGTCGCGACACCTGTCCCGTGATGGCGACCATGGGGACGGAGTCGAGCAACGCGTCTGCGAGCGCAGA	4598
	GACAGGTGTCGCGACGC	4599
	GCGTCGCGACACCTGTC	4600
Sulfonylurea Resistance ALS *Zea mays* Pro165Gln CCG-CAG	CTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGCCATCACGGGACAGGTGCAGCGACGCATGATTGGCACCGACGCCTTTCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4601
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGTGCCAATCATGCGTCGCTGCACCTGTCCCGTGATGGCGACCATGGGGACGGAGTCGAGCAACGCGTCTGCGAGCGCAG	4602
	ACAGGTGCAGCGACGCA	4603
	TGCGTCGCTGCACCTGT	4604
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAT	GGCCGTACCTCTTGGATATAATCGTCCCGCACCAGGAGCATGTGTTGCCTATGATCCCTAATGGTGGGGCTTTCAAGGATATGATCCTGGATGGTGATGGCAGGACTGTGTATTGATCCGT	4605
	ACGGATCAATACACAGTCCTGCCATCACCATCCAGGATCATATCCTTGAAAGCCCCACCATTAGGGATCATAGGCAACACATGCTCCTGGTGCGGGACGATTATATCCAAGAGGTACGGCC	4606
	GATCCCTAATGGTGGGG	4607
	CCCCACCATTAGGGATC	4608
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGATCACTGGTCAAGTCTCTCGTCGGATGATCGGTACCGATGCTTTCCAGGAAACTCCAATTGTTGAGGTAACAAGGT	4609
	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTACCGATCATCCGACGAGAGACTTGACCAGTGATCGCCACGAGAGGGATACTATCGAGCATTGCATCAGCGAGACCACT	4610
	GTCAAGTCTCTCGTCGG	4611
	CCGACGAGAGACTTGAC	4612
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGATCACTGGTCAAGTCCAACGTCGGATGATCGGTACCGATGCTTTCCAGGAAACTCCAATTGTTGAGGTAACAAGGTC	4613
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTACCGATCATCCGACGTTGGACTTGACCAGTGATCGCCACGAGAGGGATACTATCGAGCATTGCATCAGCGAGACCAC	4614
	TCAAGTCCAACGTCGGA	4615

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACG**TT**GGACTTGA	4616
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGATCACTGGTCAAGTCC**AG**CGTCGGATGATCGGTACCGATGCTTTCCAGGAAACTCCAATTGTTGAGGTAACAAGGTC	4617
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTACCGATCATCCGACG**CT**GGACTTGACCAGTGATCGCCACGAGAGGGATACTATCGAGCATTGCATCAGCGAGACCAC	4618
	TCAAGTCC**AG**CGTCGGA	4619
	TCCGACG**CT**GGACTTGA	4620
Imidazolinone Resistance ALS *Gossypium hirsutum* Ser642Asn AGT-AAT	GACCTTACTTGTTGGATGTGATTGTCCCACATCAAGAACATGTCCTGCCTATGATCCCCA**A**TGGAGGGGCTTTCAAAGATGTGATCACAGAGGGTGATGGAAGAACACAATATTGACCTCA	4621
	TGAGGTCAATATTGTGTTCTTCCATCACCCTCTGTGATCACATCTTTGAAAGCCCCTCCA**T**TGGGGATCATAGGCAGGACATGTTCTTGATGTGGGACAATCACATCCAACAAGTAAGGTC	4622
	GATCCCCA**A**TGGAGGGG	4623
	CCCCTCCA**T**TGGGGATC	4624
Sulfonylurea Resistance ALS *Amaranthus powellii* Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCATTACTGGGCAAGTT**T**CCCGGCGTATGATTGGTACTGATGCTTTTCAAGAGACTCCAATTGTTGAGGTAACTCGAT	4625
	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACCAATCATACGCCGGG**A**AACTTGCCCAGTAATGGCGACAAGAGGGACTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4626
	GGCAAGTT**T**CCCGGCGT	4627
	ACGCCGGG**A**AACTTGCC	4628
Sulfonylurea Resistance ALS *Amaranthus powellii* Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCATTACTGGGCAAGTTC**AA**CGGCGTATGATTGGTACTGATGCTTTTCAAGAGACTCCAATTGTTGAGGTAACTCGATC	4629
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACCAATCATACGCCG**TT**GAACTTGCCCAGTAATGGCGACAAGAGGGACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4630
	GCAAGTTC**AA**CGGCGTA	4631
	TACGCCG**TT**GAACTTGC	4632
Sulfonylurea Resistance ALS *Amaranthus powellii* Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCATTACTGGGCAAGTTC**AG**CGGCGTATGATTGGTACTGATGCTTTTCAAGAGACTCCAATTGTTGAGGTAACTCGATC	4633
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACCAATCATACGCCG**CT**GAACTTGCCCAGTAATGGCGACAAGAGGGACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4634

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCAAGTTCAGCGGCGTA	4635
	TACGCCGCTGAACTTGC	4636
Imidazolinone Resistance ALS *Amaranthus powellii* Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGCTGCCTATGATCCCTAACGGTGCCGCCTTCAAGGACACCATAACAGAGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4637
	ACCAACTAATAAGCCCTTCTTCCATCACCCTCTGTTATGGTGTCCTTGAAGGCGGCACCGTTAGGGATCATAGGCAGCACATGCTCCTGATGTGGTACGATTACATCCAGCAGATACGGTC	4638
	GATCCCTAACGGTGCCG	4639
	CGGCACCGTTAGGGATC	4640

Table 12

Genome-Altering Oligos Conferring Porphyric Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Porphyric Herbicide Resistant PPO *Arabidopsis thaliana* Val365Met GTT-ATG	TCTTGCGCCCTCTTTCTGAATCTGCTGCAAATGCACTCTCAAAACT ATATTACCCACCA**A**T**G**GCAGCAGTATCTATCTCGTACCCGAAAGA AGCAATCCGAACAGAATGTTTGATAGATGG	4641
	CCATCTATCAAACATTCTGTTCGGATTGCTTCTTTCGGGTACGAGA TAGATACTGCTG**C**CA**T**TGGTGGGTAATATAGTTTTGAGAGTGCATT TGCAGCAGATTCAGAAAGAGGGCGCAAGA	4642
	CCCACCA**A**T**G**GCAGCAG	4643
	CTGCTGC**C**A**T**TGGTGGG	4644
Porphyric Herbicide Resistant PPO *Nicotiana tabacum* Val376Met GTT-ATG	TATTACGTCCTCTTTCGGTTGCCGCAGCAGATGCACTTTCAAATTT CTACTATCCCCCA**A**T**G**GGAGCAGTCACAATTTCATATCCTCAAGAA GCTATTCGTGATGAGCGTCTGGTTGATGG	4645
	CCATCAACCAGACGCTCATCACGAATAGCTTCTTGAGGATATGAA ATTGTGACTGCTCC**C**A**T**TGGGGGATAGTAGAAATTTGAAAGTGCA TCTGCTGCGGCAACCGAAAGAGGACGTAATA	4646
	TCCCCCA**A**T**G**GGAGCAG	4647
	CTGCTCC**C**A**T**TGGGGGA	4648
Porphyric Herbicide Resistant PPO *Cichorium intybus* Val383Met GTT-ATG	TGTTGCGTCCGCTTTCGTTGGGTGCAGCAGATGCATTGTCAAAAT TTTATTATCCTCCG**A**T**G**GCAGCTGTATCAATTTCATATCCAAAAGA CGCAATTCGTGCTGACCGGCTGATTGATGG	4649
	CCATCAATCAGCCGGTCAGCACGAATTGCGTCTTTTGGATATGAA ATTGATACAGCTGC**C**A**T**CGGAGGATAATAAAATTTTGACAATGCAT CTGCTGCACCCAACGAAAGCGGACGCAACA	4650
	TCCTCCG**A**T**G**GCAGCTG	4651
	CAGCTGC**C**A**T**CGGAGGA	4652
Porphyric Herbicide Resistant PPO *Spinacia oleracea* Val390Met GTT-ATG	TCCTTCGTCCACTTTCAGATGTCGCCGCAGAATCTCTTTCAAAATT TCATTATCCACCA**A**T**G**GCAGCTGTGTCACTTTCCTATCCTAAAGAA GCAATTAGATCAGAGTGCTTGATTGACGG	4653
	CCGTCAATCAAGCACTCTGATCTAATTGCTTCTTTAGGATAGGAAA GTGACACAGCTGC**C**A**T**TGGTGGATAATGAAATTTTGAAAGAGATTC TGCGGCGACATCTGAAAGTGGACGAAGGA	4654
	TCCACCA**A**T**G**GCAGCTG	4655
	CAGCTGC**C**A**T**TGGTGGA	4656

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Porphyric Herbicide Resistant PPO *Zea mays* Val363Met GTT-ATG	TTTTGCGTCCACTTTCAAGCGATGCTGCAGATGCTCTATCAAGATT CTATTATCCACCGATGGCTGCTGTAACTGTTTCGTATCCAAAGGAA GCAATTAGAAAAGAATGCTTAATTGATGG	4657
	CCATCAATTAAGCATTCTTTTCTAATTGCTTCCTTTGGATACGAAAC AGTTACAGCAGCCATCGGTGGATAATAGAATCTTGATAGAGCATC TGCAGCATCGCTTGAAAGTGGACGCAAAA	4658
	TCCACCGATGGCTGCTG	4659
	CAGCAGCCATCGGTGGA	4660
Porphyric Herbicide Resistant PPO *Oryza sativa* Val364Met GTT-ATG	TCTTGCGGCCACTTTCAAGTGATGCAGCAGATGCTCTGTCAATATT CTATTATCCACCAATGGCTGCTGTAACTGTTTCATATCCAAAAGAA GCAATTAGAAAAGAATGCTTAATTGACGG	4661
	CCGTCAATTAAGCATTCTTTTCTAATTGCTTCTTTTGGATATGAAAC AGTTACAGCAGCCATTGGTGGATAATAGAATATTGACAGAGCATCT GCTGCATCACTTGAAAGTGGCCGCAAGA	4662
	TCCACCAATGGCTGCTG	4663
	CAGCAGCCATTGGTGGA	4664
Porphyric Herbicide Resistant PPO *Chlamydomonas reinhardtii* Val389Met GTG-ATG	CTGGTCAAGGAGCAGGCGCCCGCCGCCGCCGAGGCCCTGGGCT CCTTCGACTACCCGCCGATGGGCGCCGTGACGCTGTCGTACCCG CTGAGCGCCGTGCGGGAGGAGCGCAAGGCCTCGG	4665
	CCGAGGCCTTGCGCTCCTCCCGCACGGCGCTCAGCGGGTACGA CAGCGTCACGGCGCCCATCGGCGGGTAGTCGAAGGAGCCCAGG GCCTCGGCGGCGGCGGGCGCCTGCTCCTTGACCAG	4666
	ACCCGCCGATGGGCGCC	4667
	GGCGCCCATCGGCGGGT	4668

Table 13

Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Arabidopsis thaliana* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTTG	4669
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAAATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	4670

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATATGCTA**C**TTTCAACA	4671
	TGTTGAAA**G**TAGCATAT	4672
Triazine Resistant D1 Protein *Nicotiana tabacum* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4673
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATGTTATAAGTTT	4674
	ATATGCTA**C**TTTCAACA	4675
	TGTTGAAA**G**TAGCATAT	4676
Triazine Resistant D1 Protein *Populus deltoides* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTTAACAACTCTCGCTCTTTACATTTCTTCTTAGCTGCTTGGCCTGTAGTAGGTATCTG	4677
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAGCGAGAGTTGTTAAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATATTATAAGTTT	4678
	ATATGCTA**C**TTTTAACA	4679
	TGTTAAAA**G**TAGCATAT	4680
Triazine Resistant D1 Protein *Petunia x hybrida* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4681
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATATTATAAGTTT	4682
	ATATGCTA**C**TTTCAACA	4683
	TGTTGAAA**G**TAGCATAT	4684
Triazine Resistant D1 Protein *Magnolia pyramidata* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4685
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCAGCTACGATATTATAAGTTT	4686
	ATATGCTA**C**TTTCAACA	4687
	TGTTGAAA**G**TAGCATAT	4688
Triazine Resistant D1 Protein *Medicago sativa* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4689
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCTGCTACAATATTATAGGTTT	4690
	ATATGCTA**C**TTTCAACA	4691

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTTGAAA**G**TAGCATAT	4692
Triazine Resistant D1 Protein *Glycine max* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCAA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCTGCTTGGCCTGTAGTAGGTATTTG	4693
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCAGCTACAATATTATAGGTTT	4694
	ATATGCAA**C**TTTCAACA	4695
	TGTTGAAA**G**TTGCATAT	4696
Triazine Resistant D1 Protein *Brassica napus* Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCT**AC**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4697
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**GT**AGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4698
	ATATGCT**AC**TTTCAACA	4699
	TGTTGAAA**GT**AGCATAT	4700
Triazine Resistant D1 Protein *Oryza sativa* Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAATCTTCCAATATGCTA**C**TTTTAACAACTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGGATTTG	4701
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAGTTGTTAAAA**G**TAGCATATTGGAAGATTAATCGGCCAAAATAACCATGAGCGGCCACAATATTATAAGTTT	4702
	ATATGCTA**C**TTTTAACA	4703
	TGTTAAAA**G**TAGCATAT	4704
Triazine Resistant D1 Protein *Zea mays* Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAATCTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGGATCTG	4705
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATTAATCGACCAAAATAACCGTGAGCAGCCACAATATTATAAGTCT	4706
	ATATGCTA**C**TTTCAACA	4707
	TGTTGAAA**G**TAGCATAT	4708
Triazine Resistant D1 Protein *Arabidopsis thaliana* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATTTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4709
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAAATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4710
	ATATGCTA**C**TTTCAACA	4711
	TGTTGAAA**G**TAGCATAT	4712

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Nicotiana tabacum* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4713
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	4714
	ATATGCTA**C**TTTCAACA	4715
	TGTTGAAA**G**TAGCATAT	4716
Triazine Resistant D1 Protein *Populus deltoides* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA**C**TTTTAACAACTCTCGCTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG	4717
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG CGAGAGTTGTTAAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCGGCTACGATATTATAAGTTT	4718
	ATATGCTA**C**TTTTAACA	4719
	TGTTAAAA**G**TAGCATAT	4720
Triazine Resistant D1 Protein *Petunia x hybrida* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4721
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4722
	ATATGCTA**C**TTTCAACA	4723
	TGTTGAAA**G**TAGCATAT	4724
Triazine Resistant D1 Protein *Magnolia pyramidata* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4725
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCAGCTACGATATTATAAGTTT	4726
	ATATGCTA**C**TTTCAACA	4727
	TGTTGAAA**G**TAGCATAT	4728
Triazine Resistant D1 Protein *Medicago sativa* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4729
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATATTATAGGTTT	4730
	ATATGCTA**C**TTTCAACA	4731
	TGTTGAAA**G**TAGCATAT	4732

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Glycine max* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCAA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCTGCTTGGCCTGTAGTAGGTATTTG	4733
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCAGCTACAATATTATAGGTTT	4734
	ATATGCAA**C**TTTCAACA	4735
	TGTTGAAA**G**TTGCATAT	4736
Triazine Resistant D1 Protein *Brassica napus* Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCT**AC**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4737
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4738
	ATATGCT**AC**TTTCAACA	4739
	TGTTGAAA**GT**AGCATAT	4740
Triazine Resistant D1 Protein *Oryza sativa* Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAATCTTCCAATATGCTA**C**TTTTAACAACTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGGATTTG	4741
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAGTTGTTAAAA**GT**AGCATATTGGAAGATTAATCGGCCAAAATAACCATGAGCGGCCACAATATTATAAGTTT	4742
	ATATGCTA**C**TTTTAACA	4743
	TGTTAAAA**G**TAGCATAT	4744
Triazine Resistant D1 Protein *Zea mays* Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAATCTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGGATCTG	4745
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATTAATCGACCAAAATAACCGTGAGCAGCCACAATATTATAAGTCT	4746
	ATATGCTA**C**TTTCAACA	4747
	TGTTGAAA**G**TAGCATAT	4748
Triazine Resistant D1 Protein *Arabidopsis thaliana* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATTTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4749
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAAATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4750
	ATATGCTA**C**TTTCAACA	4751
	TGTTGAAA**G**TAGCATAT	4752

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Picea abies* Ser264Thr AGT-ACT	AAACCTACAATATTGTGGCTGCTCACGGTTATTTCGGCCGATTGATCTTCCAGTATGCTA**C**TTTCAACAACTCCCGTTCTTTACATTTCTTCTTAGCTGCTTGGCCCGTAGCAGGTATCTG	4753
	CAGATACCTGCTACGGGCCAAGCAGCTAAGAAGAAATGTAAAGAACGGGAGTTGTTGAAA**G**TAGCATACTGGAAGATCAATCGGCCGAAATAACCGTGAGCAGCCACAATATTGTAGGTTT	4754
	GTATGCTA**C**TTTCAACA	4755
	TGTTGAAA**G**TAGCATAC	4756
Triazine Resistant D1 Protein *Vicia faba* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAATTCTCGCTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4757
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAGCGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATATTATAGGTTT	4758
	ATATGCTA**C**TTTCAACA	4759
	TGTTGAAA**G**TAGCATAT	4760
Triazine Resistant D1 Protein *Hordeum vulgare* Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCATGGTTATTTTGGCCGATTAATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGAATCTG	4761
	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAATAACCATGAGCAGCCACAATATTATAAGTCT	4762
	ATATGCTACTTTCAACA	4763
	TGTTGAAAGTAGCATAT	4764
Triazine Resistant D1 Protein *Triticum aestivum* Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCTGCTCATGGTTATTTTGGCCGATTAATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCTTGGCTGCTTGGCCTGTAGTAGGAATCTG	4765
	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATTAATCGGCCAAAATAACCATGAGCAGCCACAATATTATAAGTTT	4766
	ATATGCTA**C**TTTCAACA	4767
	TGTTGAAA**G**TAGCATAT	4768
Triazine Resistant D1 Protein *Vigna unguiculata* Ser264Thr AGT-ACT	AAACTTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTAATCTTCCAATATGCAA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATTTG	4769
	CAAATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TTGCATATTGGAAGATTAATCGGCCAAAATAACCATGAGCAGCTACAATATTATAAGTTT	4770
	ATATGCAA**C**TTTCAACA	4771
	TGTTGAAA**G**TTGCATAT	4772

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Lotus japonicus* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCAA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCTTAGCTGCTTGGCCTGTTGTAGGTATCTG	4773
	CAGATACCTACAACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAACGAGAGTTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATATTATAGGTTT	4774
	ATATGCAA**C**TTTCAACA	4775
	TGTTGAAA**G**TTGCATAT	4776
Triazine Resistant D1 Protein *Sinapis alba* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG	4777
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT	4778
	ATATGCTA**C**TTTCAACA	4779
	TGTTGAAA**G**TAGCATAT	4780
Triazine Resistant D1 Protein *Pisum sativum* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAATTCTCGCTCTTTACATTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4781
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAGCGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCGTGAGCAGCTACAATATTATAGGTTT	4782
	ATATGCTA**C**TTTCAACA	4783
	TGTTGAAA**G**TAGCATAT	4784
Triazine Resistant D1 Protein *Spinacia oleracea* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGTCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCTTAGCTGCTTGGCCTGTAGTAGGTATTTG	4785
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGACCAAAATAACCATGAGCAGCTACGATATTATAAGTTT	4786
	ATATGCTA**C**TTTCAACA	4787
	TGTTGAAA**G**TAGCATAT	4788
Triazine Resistant D1 Protein *Nicotiana debneyi* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4789
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATGTTATAAGTTT	4790
	ATATGCTA**C**TTTCAACA	4791
	TGTTGAAA**G**TAGCATAT	4792

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Solanum nigrum* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4793
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATATTATAAGTTT	4794
	ATATGCTA**C**TTTCAACA	4795
	TGTTGAAA**G**TAGCATAT	4796
Triazine Resistant D1 Protein *Nicotiana plumbaginifolia* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGATCTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCCTAGCTGCTTGGCCTGTAGTAGGTATCTG	4797
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAACGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAATAACCATGAGCGGCTACGATGTTATAAGTTT	4798
	ATATGCTA**C**TTTCAACA	4799
	TGTTGAAA**G**TAGCATAT	4800

Example 6
Engineering male- or female-sterile plants

Flower development in distantly related dicot plant species is increasingly better understood and appears to be regulated by a family of genes which encode regulatory proteins. These genes include, for example, *AGAMOUS* (*AG*), *APETALA1* (*AP1*), and *APETALA3* (*AP3*) and *PISTILLATA* (*PI*) in *Arabidopsis thaliana*, and *DEFICIENS A* (*DEFA*), *GLOBOSA* (*GLO*), *SQUAMOSA* (*SQUA*), and *PLENA* (*PLE*) in *Antirrhinum majus*. Genetic studies have shown that the *DEFA*, *GLO* and *AP3* genes are essential for petal and stamen development. Sequence analysis of these genes revealed that the gene products contain a conserved MADS box region, a DNA-binding domain. Using these clones as probes, MADS box genes have also been isolated from other species including tomato, tobacco, petunia, *Brassica napus*, and maize.

Altering the expression of these genes results in altered floral morphology. For example, mutations in *AP3* and *PI* result in male-sterile flowers because petals develop in place of stamens.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer altered floral structures in plants.

Table 14
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AP3 *Arabidopsis thaliana* Arg3Term AGA-TGA	TTGTCCTCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGTGAGGGAAGATCCAGATCAAGAGGATAGAGAACCAGACAAACAGACAAGTGACGTATTCAA	4801
	TTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTCTTGATCTGGATCTTCCCTCACGCCATATTCTTCTCTCTTTGTTTAATCTTTTTGTTGAAGAGATTTGGTGGAGAGGACAA	4802
	ATATGGCGTGAGGGAAG	4803
	CTTCCCTCACGCCATAT	4804
Male-sterile AP3 *Arabidopsis thaliana* Lys5Term AAG-TAG	TCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAGGGTAGATCCAGATCAAGAGGATAGAGAACCAGACAAACAGACAAGTGACGTATTCAAAGAGAA	4805
	TTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTCTTGATCTGGATCTACCCTCTCGCCATATTCTTCTCTCTTTGTTTAATCTTTTTGTTGAAGAGATTTGGTGGAGA	4806
	CGAGAGGGTAGATCCAG	4807

	CTGGATCT**A**CCCTCTCG	4808
Male-sterile AP3 *Arabidopsis thaliana* Gln7Term CAG-TAG	CCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAGGGAAGATC**T**AGATCAAGAGGATAGAGAACCAGACAAACAGACAAGTGACGTATTCAAAGAGAAGGAATG	4809
	CATTCCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTCTTGATCT**A**GATCTTCCCTCTCGCCATATTCTTCTCTCTTTGTTTAATCTTTTTGTTGAAGAGATTTGG	4810
	GGAAGATC**T**AGATCAAG	4811
	CTTGATCT**A**GATCTTCC	4812
Male-sterile AP3 *Arabidopsis thaliana* Lys9Term AAG-TAG	CTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAGGGAAGATCCAGATC**T**AGAGGATAGAGAACCAGACAAACAGACAAGTGACGTATTCAAAGAGAAGGAATGGTTTAT	4813
	ATAAACCATTCCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTCT**A**GATCTGGATCTTCCCTCTCGCCATATTCTTCTCTCTTTGTTTAATCTTTTTGTTGAAGAG	4814
	TCCAGATC**T**AGAGGATA	4815
	TATCCTCT**A**GATCTGGA	4816
Male-sterile AP3 *Brassica oleracea* Lys23Term AAG-TAG	AGAGGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAAGTGACGTATTCT**T**AGAGAAGAAATGGTTTGTTCAAGAAAGCTCACGAGCTTACAGTTTTATGTGATGCTAGGG	4817
	CCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTTGAACAAACCATTTCTTCTCT**A**AGAATACGTCACTTGTCGGTTGGTCTGGTTCTCTATCCTCTTGATCTGGATCTTCCCTCT	4818
	CGTATTCT**T**AGAGAAGA	4819
	TCTTCTCT**A**AGAATACG	4820
Male-sterile AP3 *Brassica oleracea* Arg24Term AGA-TGA	GGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAAGTGACGTATTCTAAG**T**GAAGAAATGGTTTGTTCAAGAAAGCTCACGAGCTTACAGTTTTATGTGATGCTAGGGTTT	4821
	AAACCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTTGAACAAACCATTTCTTC**A**CTTAGAATACGTCACTTGTCGGTTGGTCTGGTTCTCTATCCTCTTGATCTGGATCTTCCC	4822
	ATTCTAAG**T**GAAGAAAT	4823
	ATTTCTTC**A**CTTAGAAT	4824
Male-sterile AP3 *Brassica oleracea* Arg25Term AGA-TGA	AAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAAGTGACGTATTCTAAGAGA**T**GAAATGGTTTGTTCAAGAAAGCTCACGAGCTTACAGTTTTATGTGATGCTAGGGTTTCGA	4825
	TCGAAACCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTTGAACAAACCATTTC**A**TCTCTTAGAATACGTCACTTGTCGGTTGGTCTGGTTCTCTATCCTCTTGATCTGGATCTT	4826
	CTAAGAGA**T**GAAATGGT	4827
	ACCATTTC**A**TCTCTTAG	4828

Male-sterile AP3 *Brassica oleracea* Leu28Term TTG-TAG	TCAAGAGGATAGAGAACCAGACCAACCGACAAGTGACGTATTCTA AGAGAAGAAATGGTT**A**GTTCAAGAAAGCTCACGAGCTTACAGTTTT ATGTGATGCTAGGGTTTCGATTATCATGTT	4829
	AACATGATAATCGAAACCCTAGCATCACATAAAACTGTAAGCTCGT GAGCTTTCTTGAAC**T**AACCATTTCTTCTCTTAGAATACGTCACTTGT CGGTTGGTCTGGTTCTCTATCCTCTTGA	4830
	AAATGGTT**A**GTTCAAGA	4831
	TCTTGAAC**T**AACCATTT	4832
Male-sterile AP3 *Brassica napus* Tyr21Term TAC-TAG	GGCTCGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAA CAGGCAGGTCACCTA**G**TCCAAGAGAAGAAATGGTTTGTTCAAGAA AGCACACGAGCTCTCTGTTCTCTGTGATGCT	4833
	AGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAAACC ATTTCTTCTCTTGGA**C**TAGGTGACCTGCCTGTTTGTTTGGTTCTCTA TCCTCTTAATCTGGATCTTCCCTCGAGCC	4834
	GTCACCTA**G**TCCAAGAG	4835
	CTCTTGGA**C**TAGGTGAC	4836
Male-sterile AP3 *Brassica napus* Lys23Term AAG-TAG	CGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGG CAGGTCACCTACTCC**T**AGAGAAGAAATGGTTTGTTCAAGAAAGCAC ACGAGCTCTCTGTTCTCTGTGATGCTAAAG	4837
	CTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAA ACCATTTCTTCTCT**A**GGAGTAGGTGACCTGCCTGTTTGTTTGGTTC TCTATCCTCTTAATCTGGATCTTCCCTCG	4838
	CCTACTCC**T**AGAGAAGA	4839
	TCTTCTCT**A**GGAGTAGG	4840
Male-sterile AP3 *Brassica napus* Arg24Term AGA-TGA	GGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAG GTCACCTACTCCAAG**T**GAAGAAATGGTTTGTTCAAGAAAGCACACG AGCTCTCTGTTCTCTGTGATGCTAAAGTTT	4841
	AAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAA CAAACCATTTCTTC**A**CTTGGAGTAGGTGACCTGCCTGTTTGTTTGG TTCTCTATCCTCTTAATCTGGATCTTCCC	4842
	ACTCCAAG**T**GAAGAAAT	4843
	ATTTCTTC**A**CTTGGAGT	4844
Male-sterile AP3 *Brassica napus* Arg25Term AGA-TGA	AAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTC ACCTACTCCAAGAGA**T**GAAATGGTTTGTTCAAGAAAGCACACGAGC TCTCTGTTCTCTGTGATGCTAAAGTTTCCA	4845
	TGGAAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTT GAACAAACCATTTC**A**TCTCTTGGAGTAGGTGACCTGCCTGTTTGTT TGGTTCTCTATCCTCTTAATCTGGATCTT	4846
	CCAAGAGA**T**GAAATGGT	4847
	ACCATTTC**A**TCTCTTGG	4848

Male-sterile DEFA *Antirrhinum majus* Arg3Term CGA-TGA	GGAGAGAAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTTGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTCACCTACTCCA	4849
	TGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAATCTGGATCTTCCCTCAAGCCATCGAACCACTACCACTACTGCTCTTGTTTTCTTCTTCCAGCTTTCCTTTCTCTCC	4850
	CGATGGCTTGAGGGAAG	4851
	CTTCCCTCAAGCCATCG	4852
Male-sterile DEFA *Antirrhinum majus* Lys5Term AAG-TAG	AAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTCGAGGGTAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTCACCTACTCCAAGAGAA	4853
	TTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAATCTGGATCTACCCTCGAGCCATCGAACCACTACCACTACTGCTCTTGTTTTCTTCTTCCAGCTTTCCTTT	4854
	CTCGAGGGTAGATCCAG	4855
	CTGGATCTACCCTCGAG	4856
Male-sterile DEFA *Antirrhinum majus* Gln7Term CAG-TAG	AAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTCGAGGGAAGATCTAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTCACCTACTCCAAGAGAAGAAATG	4857
	CATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAATCTAGATCTTCCCTCGAGCCATCGAACCACTACCACTACTGCTCTTGTTTTCTTCTTCCAGCTT	4858
	GGAAGATCTAGATTAAG	4859
	CTTAATCTAGATCTTCC	4860
Male-sterile DEFA *Antirrhinum majus* Lys9Term AAG-TAG	GAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTCGAGGGAAGATCCAGATTTAGAGGATAGAGAACCAAACAAACAGGCAGGTCACCTACTCCAAGAGAAGAAATGGTTTGT	4861
	ACAAACCATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTAAATCTGGATCTTCCCTCGAGCCATCGAACCACTACCACTACTGCTCTTGTTTTCTTCTTC	4862
	TCCAGATTTAGAGGATA	4863
	TATCCTCTAAATCTGGA	4864
Male-sterile AP3 *Nicotiana tabacum* Lys5Term AAG-TAG	TCAGTAATTCTTAAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGCTCGTGGGTAGATCCAGATCAAGAGAATAGAGAACCAAACAAACAGACAAGTCACTTATTCTAAGAGAA	4865
	TTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGGTTCTCTATTCTCTTGATCTGGATCTACCCACGAGCCATAGTTTTTTTTTCTTTTTGCTCAAAGTTTGAGATCTTAAGAATTACTGA	4866
	CTCGTGGGTAGATCCAG	4867
	CTGGATCTACCCACGAG	4868

Male-sterile AP3 *Nicotiana tabacum* Gln7Term CAG-TAG	ATTCTTAAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGCTCGTGGGAAGATC**T**AGATCAAGAGAATAGAGAACCAAACAAACAGACAAGTCACTTATTCTAAGAGAAGAAATG	4869
	CATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGGTTCTCTATTCTCTTGATCT**A**GATCTTCCCACGAGCCATAGTTTTTTTTTCTTTTTGCTCAAAGTTTGAGATCTTAAGAAT	4870
	GGAAGATC**T**AGATCAAG	4871
	CTTGATCT**A**GATCTTCC	4872
Male-sterile AP3 *Nicotiana tabacum* Lys9Term AAG-TAG	AAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGCTCGTGGGAAGATCCAGATC**T**AGAGAATAGAGAACCAAACAAACAGACAAGTCACTTATTCTAAGAGAAGAAATGGACTTT	4873
	AAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGGTTCTCTATTCTCT**A**GATCTGGATCTTCCCACGAGCCATAGTTTTTTTTTCTTTTTGCTCAAAGTTTGAGATCTT	4874
	TCCAGATC**T**AGAGAATA	4875
	TATTCTCT**A**GATCTGGA	4876
Male-sterile AP3 *Nicotiana tabacum* Arg10Term AGA-TGA	ATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGCTCGTGGGAAGATCCAGATCAAG**T**GAATAGAGAACCAAACAAACAGACAAGTCACTTATTCTAAGAGAAGAAATGGACTTTTCA	4877
	TGAAAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGGTTCTCTATTC**A**CTTGATCTGGATCTTCCCACGAGCCATAGTTTTTTTTTCTTTTTGCTCAAAGTTTGAGAT	4878
	AGATCAAG**T**GAATAGAG	4879
	CTCTATTC**A**CTTGATCT	4880
Male-sterile AP3 *Medicago sativa* Tyr21Term TAC-TAG	GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAAGTAACTTA**G**TCAAAACGAAGGGATGGTCTTTTCAAGAAGGCCAATGAGCTCACTGTTCTTTGTGATGCT	4881
	AGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGACCATCCCTTCGTTTTGA**C**TAAGTTACTTGTCTGTTCGTTGTGTTCTCTATTCTCTTGATCTGGATCTTTCCTCGAGCC	4882
	GTAACTTA**G**TCAAAACG	4883
	CGTTTTGA**C**TAAGTTAC	4884
Male-sterile AP3 *Medicago sativa* Ser22Term TCA-TGA	CTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAAGTAACTTACT**G**AAAACGAAGGGATGGTCTTTTCAAGAAGGCCAATGAGCTCACTGTTCTTTGTGATGCTAA	4885
	TTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGACCATCCCTTCGTTTT**C**AGTAAGTTACTTGTCTGTTCGTTGTGTTCTCTATTCTCTTGATCTGGATCTTTCCTCGAG	4886
	AACTTACT**G**AAAACGAA	4887
	TTCGTTTT**C**AGTAAGTT	4888

Male-sterile AP3 *Medicago sativa* Lys23Term AAA-TAA	CGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAAGTAACTTACTCA**T**AACGAAGGGATGGTCTTTTCAAGAAGGCCAATGAGCTCACTGTTCTTTGTGATGCTAAGG	4889
	CCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGACCATCCCTTCGTT**A**TGAGTAAGTTACTTGTCTGTTCGTTGTGTTCTCTATTCTCTTGATCTGGATCTTTCCTCG	4890
	CTTACTCA**T**AACGAAGG	4891
	CCTTCGTT**A**TGAGTAAG	4892
Male-sterile AP3 *Medicago sativa* Arg24Term CGA-TGA	GGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAAGTAACTTACTCAAAA**T**GAAGGGATGGTCTTTTCAAGAAGGCCAATGAGCTCACTGTTCTTTGTGATGCTAAGGTTT	4893
	AAACCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGACCATCCCTTC**A**TTTTGAGTAAGTTACTTGTCTGTTCGTTGTGTTCTCTATTCTCTTGATCTGGATCTTTCC	4894
	ACTCAAAA**T**GAAGGGAT	4895
	ATCCCTTC**A**TTTTGAGT	4896
Male-sterile DEF4 *Solanum tuberosum* Tyr21Term TAT-TAG	GGCTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAAGTGACTTA**G**TCAAAGAGAAGAAATGGGCTATTCAAGAAGGCTAATGAACTTACAGTTCTTTGTGATGCT	4897
	AGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCATTTCTTCTCTTTGA**C**TAAGTCACTTGCCTATTTGTTTGGTTTTCTATTTTCTTGATCTGGATCTTACCACGAGCC	4898
	GTGACTTA**G**TCAAAGAG	4899
	CTCTTTGA**C**TAAGTCAC	4900
Male-sterile DEF4 *Solanum tuberosum* Ser22Term TCA-TGA	CTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAAGTGACTTATT**G**AAAGAGAAGAAATGGGCTATTCAAGAAGGCTAATGAACTTACAGTTCTTTGTGATGCTAA	4901
	TTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCATTTCTTCTCTTT**C**AATAAGTCACTTGCCTATTTGTTTGGTTTTCTATTTTCTTGATCTGGATCTTACCACGAG	4902
	GACTTATT**G**AAAGAGAA	4903
	TTCTCTTT**C**AATAAGTC	4904
Male-sterile DEF4 *Solanum tuberosum* Lys23Term AAG-TAG	CGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAAGTGACTTATTCA**T**AGAGAAGAAATGGGCTATTCAAGAAGGCTAATGAACTTACAGTTCTTTGTGATGCTAAAG	4905
	CTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCATTTCTTCTCT**A**TGAATAAGTCACTTGCCTATTTGTTTGGTTTTCTATTTTCTTGATCTGGATCTTACCACG	4906
	CTTATTCA**T**AGAGAAGA	4907
	TCTTCTCT**A**TGAATAAG	4908

Male-sterile DEF4 *Solanum tuberosum* Arg24Term AGA-TGA	GGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAAGTGACTTATTCAAAGTGAAGAAATGGGCTATTCAAGAAGGCTAATGAACTTACAGTTCTTTGTGATGCTAAAGTTT	4909
	AAACTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCATTTCTTCACTTTGAATAAGTCACTTGCCTATTTGTTTGGTTTTCTATTTTCTTGATCTGGATCTTACC	4910
	ATTCAAAGTGAAGAAAT	4911
	ATTTCTTCACTTTGAAT	4912
Male-sterile AP3 *Lycopersicon esculentum* Gly27Term GGA-TGA	GCTAATGAACTTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTACTTGAAAACTTCATGAGTTTATAAGTCCCTCTATCACGACCAAACAATTGTTCGATCTGTACC	4913
	GGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAACTCATGAAGTTTTCAAGTACTAGAAATCATAACAATTGAAACTTTAGCATCACAAAGAACAGTAAGTTCATTAGC	4914
	CTAGTACTTGAAAACTT	4915
	AAGTTTTCAAGTACTAG	4916
Male-sterile AP3 *Lycopersicon esculentum* Lys28Term AAA-TAA	AATGAACTTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTACTGGATAACTTCATGAGTTTATAAGTCCCTCTATCACGACCAAACAATTGTTCGATCTGTACCAGA	4917
	TCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAACTCATGAAGTTATCCAGTACTAGAAATCATAACAATTGAAACTTTAGCATCACAAAGAACAGTAAGTTCATT	4918
	GTACTGGATAACTTCAT	4919
	ATGAAGTTATCCAGTAC	4920
Male-sterile AP3 *Lycopersicon esculentum* Glu31Term GAG-TAG	ACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTACTGGAAAACTTCATTAGTTTATAAGTCCCTCTATCACGACCAAACAATTGTTCGATCTGTACCAGAAGACTATTG	4921
	CAATAGTCTTCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAACTAATGAAGTTTTCCAGTACTAGAAATCATAACAATTGAAACTTTAGCATCACAAAGAACAGT	4922
	AACTTCATTAGTTTATA	4923
	TATAAACTAATGAAGTT	4924
Male-sterile AP3 *Lycopersicon esculentum* Lys40Term AAA-TAA	ATTGTTATGATTTCTAGTACTGGAAAACTTCATGAGTTTATAAGTCCCTCTATCACGACCTAACAATTGTTCGATCTGTACCAGAAGACTATTGGAGTTGATATTTGGACTACTCACTATG	4925
	CATAGTGAGTAGTCCAAATATCAACTCCAATAGTCTTCTGGTACAGATCGAACAATTGTTAGGTCGTGATAGAGGGACTTATAAACTCATGAAGTTTTCCAGTACTAGAAATCATAACAAT	4926
	TCACGACCTAACAATTG	4927
	CAATTGTTAGGTCGTGA	4928

Male-sterile AP3 *Triticum aestivum* Tyr21Term TAC-TAG	GGGGCGGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCA ACAGGCAGGTGACCTA**G**TCCAAGCGCCGGTCGGGGATCATGAAG AAGGCGCGGGAGCTCACCGTGCTCTGCGACGCC	4929
	GGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATGATCC CCGACCGGCGCTTGGA**C**TAGGTCACCTGCCTGTTGGTGGCGTTC TCGATCCGCTTTATCTCAATCTTCCCCCGCCCC	4930
	GTGACCTA**G**TCCAAGCG	4931
	CGCTTGGA**C**TAGGTCAC	4932
Male-sterile AP3 *Triticum aestivum* Lys23Term AAG-TAG	CGGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAG GCAGGTGACCTACTCC**T**AGCGCCGGTCGGGGATCATGAAGAAGG CGCGGGAGCTCACCGTGCTCTGCGACGCCCAGG	4933
	CCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATG ATCCCCGACCGGCGCT**A**GGAGTAGGTCACCTGCCTGTTGGTGGC GTTCTCGATCCGCTTTATCTCAATCTTCCCCCG	4934
	CCTACTCC**T**AGCGCCGG	4935
	CCGGCGCT**A**GGAGTAGG	4936
Male-sterile AP3 *Triticum aestivum* Ser26Term TCG-TAG	TTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCT ACTCCAAGCGCCGGT**A**GGGGATCATGAAGAAGGCGCGGGAGCTC ACCGTGCTCTGCGACGCCCAGGTCGCCATCAT	4937
	ATGATGGCGACCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGC CTTCTTCATGATCCCC**T**ACCGGCGCTTGGAGTAGGTCACCTGCCT GTTGGTGGCGTTCTCGATCCGCTTTATCTCAA	4938
	GCGCCGGT**A**GGGGATCA	4939
	TGATCCCC**T**ACCGGCGC	4940
Male-sterile AP3 *Triticum aestivum* Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCCAAGCG CCGGTCGGGGATCATG**T**AGAAGGCGCGGGAGCTCACCGTGCTCT GCGACGCCCAGGTCGCCATCATCATGTTCTCCT	4941
	AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG AGCTCCCGCGCCTTCT**A**CATGATCCCCGACCGGCGCTTGGAGTA GGTCACCTGCCTGTTGGTGGCGTTCTCGATCCG	4942
	GGATCATG**T**AGAAGGCG	4943
	CGCCTTCT**A**CATGATCC	4944
Male-sterile Silky1 *Zea mays* Tyr21Term TAC-TAG	GGGGCGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCA ACCGCCAGGTGACCTA**G**TCCAAGCGCCGGACGGGGATCATGAAG AAGGCACGCGAGCTCACCGTGCTCTGCGACGCC	4945
	GGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATGATCC CCGTCCGGCGCTTGGA**C**TAGGTCACCTGGCGGTTGGTGGCGTTC TCGATCCGCTTGATCTCGATCTTGCCGCGCCCC	4946
	GTGACCTA**G**TCCAAGCG	4947
	CGCTTGGA**C**TAGGTCAC	4948

Male-sterile Silky1 *Zea mays* Lys23Term AAG-TAG	CGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCTAGCGCCGGACGGGGATCATGAAGAAGGCACGCGAGCTCACCGTGCTCTGCGACGCCCAGG	4949
	CCTGGGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATGATCCCCGTCCGGCGCTAGGAGTAGGTCACCTGGCGGTTGGTGGCGTTCTCGATCCGCTTGATCTCGATCTTGCCGCG	4950
	CCTACTCCTAGCGCCGG	4951
	CCGGCGCTAGGAGTAGG	4952
Male-sterile Silky1 *Zea mays* Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCGCCGGACGGGGATCATGTAGAAGGCACGCGAGCTCACCGTGCTCTGCGACGCCCAGGTCGCCATCATCATGTTCTCCT	4953
	AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTACATGATCCCCGTCCGGCGCTTGGAGTAGGTCACCTGGCGGTTGGTGGCGTTCTCGATCCG	4954
	GGATCATGTAGAAGGCA	4955
	TGCCTTCTACATGATCC	4956
Male-sterile Silky1 *Zea mays* Lys31Term AAG-TAG	ATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCGCCGGACGGGGATCATGAAGTAGGCACGCGAGCTCACCGTGCTCTGCGACGCCCAGGTCGCCATCATCATGTTCTCCTCCA	4957
	TGGAGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTACTTCATGATCCCCGTCCGGCGCTTGGAGTAGGTCACCTGGCGGTTGGTGGCGTTCTCGAT	4958
	TCATGAAGTAGGCACGC	4959
	GCGTGCCTACTTCATGA	4960
Male-sterile AP3 *Oryza sativa* Lys5Term AAG-TAG	GCTAGCTGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCTAGATCGAGATCAAGCGGATCGAGAACGCGACCAACAGGCAGGTGACCTACTCGAAGCGCC	4961
	GGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCGCGTTCTCGATCCGCTTGATCTCGATCTAGCCCCTCCCCATGGCCGCCCCCTGCAGCAGCTATCTCTCTCGCCGGACAATGCAGCTAGC	4962
	GGAGGGGCTAGATCGAG	4963
	CTCGATCTAGCCCCTCC	4964
Male-sterile AP3 *Oryza sativa* Glu7Term GAG-TAG	TGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCAAGATCTAGATCAAGCGGATCGAGAACGCGACCAACAGGCAGGTGACCTACTCGAAGCGCCGCACGG	4965
	CCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCGCGTTCTCGATCCGCTTGATCTAGATCTTGCCCCTCCCCATGGCCGCCCCCTGCAGCAGCTATCTCTCTCGCCGGACAATGCA	4966
	GCAAGATCTAGATCAAG	4967
	CTTGATCTAGATCTTGC	4968

Male-sterile AP3 *Oryza sativa* Lys9Term AAG-TAG	GTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCAAGATCGAGATCTAGCGGATCGAGAACGCGACCAACAGGCAGGTGACCTACTCGAAGCGCCGCACGGGGATCA	4969
	TGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCGCGTTCTCGATCCGCTAGATCTCGATCTTGCCCCTCCCCATGGCCGCCCCCTGCAGCAGCTATCTCTCTCGCCGGAC	4970
	TCGAGATCTAGCGGATC	4971
	GATCCGCTAGATCTCGA	4972
Male-sterile AP3 *Oryza sativa* Glu12Term GAG-TAG	GAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCAAGATCGAGATCAAGCGGATCTAGAACGCGACCAACAGGCAGGTGACCTACTCGAAGCGCCGCACGGGGATCATGAAGAAGG	4973
	CCTTCTTCATGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCGCGTTCTAGATCCGCTTGATCTCGATCTTGCCCCTCCCCATGGCCGCCCCCTGCAGCAGCTATCTCTC	4974
	AGCGGATCTAGAACGCG	4975
	CGCGTTCTAGATCCGCT	4976

Table 15
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Arabidopsis thaliana* Tyr35Term TAC-TAG	TCTGTACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAGCAATCACGGCGTAGCAATCGGAGCTAGGAGGAGATTCCTCTCCCTTGAGGAAATCTGGGAGAGGAAAGATCGAA	4977
	TTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCCTCCTAGCTCCGATTGCTACGCCGTGATTGCTGCTCCAAAGCCAAAAACGTTTAGGGCAAAATTTGATTAGTACAGA	4978
	ACGGCGTAGCAATCGGA	4979
	TCCGATTGCTACGCCGT	4980
Male-sterile AG *Arabidopsis thaliana* Gln36Term CAA-TAA	CTGTACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAGCAATCACGGCGTACTAATCGGAGCTAGGAGGAGATTCCTCTCCCTTGAGGAAATCTGGGAGAGGAAAGATCGAAA	4981
	TTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCCTCCTAGCTCCGATTAGTACGCCGTGATTGCTGCTCCAAAGCCAAAAACGTTTAGGGCAAAATTTGATTAGTACAG	4982
	CGGCGTACTAATCGGAG	4983
	CTCCGATTAGTACGCCG	4984

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Arabidopsis thaliana* Ser37Term TCG-TAG	ACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAGCAATCACGGCGTACCAATAGGAGCTAGGAGGAGATTCCTCTCCCTTGAGGAAATCTGGGAGAGGAAAGATCGAAATCAA	4985
	TTGATTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCCTCCTAGCTCCTATTGGTACGCCGTGATTGCTGCTCCAAAGCCAAAAACGTTTAGGGCAAAATTTGATTAGT	4986
	GTACCAATAGGAGCTAG	4987
	CTAGCTCCTATTGGTAC	4988
Male-sterile AG *Arabidopsis thaliana* Glu38Term GAG-TAG	TAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAGCAATCACGGCGTACCAATCGTAGCTAGGAGGAGATTCCTCTCCCTTGAGGAAATCTGGGAGAGGAAAGATCGAAATCAAAC	4989
	GTTTGATTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCCTCCTAGCTACGATTGGTACGCCGTGATTGCTGCTCCAAAGCCAAAAACGTTTAGGGCAAAATTTGATTA	4990
	ACCAATCGTAGCTAGGA	4991
	TCCTAGCTACGATTGGT	4992
Male-sterile AG *Brassica napus* Glu3Term GAA-TAA	CTCTCCCACTTCTTTTCGGTGGTTTATTCATTTGGTGACGATATCACAGAAGCAATGGATTAAGGTGGGAGTAGTCACGATGCAGAGAGTAGCAAGAAGATAGGTAGAGGGAAGATAGAGA	4993
	TCTCTATCTTCCCTCTACCTATCTTCTTGCTACTCTCTGCATCGTGACTACTCCCACCTTAATCCATTGCTTCTGTGATATCGTCACCAAATGAATAAACCACCGAAAAGAAGTGGGAGAG	4994
	CAATGGATTAAGGTGGG	4995
	CCCACCTTAATCCATTG	4996
Male-sterile AG *Brassica napus* Glu11Term GAG-TAG	TATTCATTTGGTGACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGATGCATAGAGTAGCAAGAAGATAGGTAGAGGGAAGATAGAGATAAAGAGGATAGAGAACACAACAA	4997
	TTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCTCTACCTATCTTCTTGCTACTCTATGCATCGTGACTACTCCCACCTTCATCCATTGCTTCTGTGATATCGTCACCAAATGAATA	4998
	ACGATGCATAGAGTAGC	4999
	GCTACTCTATGCATCGT	5000
Male-sterile AG *Brassica napus* Lys14Term AAG-TAG	GGTGACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGATGCAGAGAGTAGCTAGAAGATAGGTAGAGGGAAGATAGAGATAAAGAGGATAGAGAACACAACAAATCGTCAAG	5001
	CTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCTCTACCTATCTTCTAGCTACTCTCTGCATCGTGACTACTCCCACCTTCATCCATTGCTTCTGTGATATCGTCACC	5002
	AGAGTAGCTAGAAGATA	5003
	TATCTTCTAGCTACTCT	5004

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Brassica napus* Lys15Term AAG-TAG	GACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGATGCAGAGAGTAGCAAG**T**AGATAGGTAGAGGGAAGATAGAGATAAAGAGGATAGAGAACACAACAAATCGTCAAGTAA	5005
	TTACTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCTCTACCTATCT**A**CTTGCTACTCTCTGCATCGTGACTACTCCCACCTTCATCCATTGCTTCTGTGATATCGTC	5006
	GTAGCAAG**T**AGATAGGT	5007
	ACCTATCT**A**CTTGCTAC	5008
Male-sterile AG *Lycopersicon esculentum* Glu4Term CAA-TAA	CAACCAAAAAACTTAAAAATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTC**T**AAAGTGATCTAACCAGAGAGATCTCACCACAAAGGAAACTAGGAAGGGGGAAAATTGAGA	5009
	TCTCAATTTTCCCCCTTCCTAGTTTCCTTTGTGGTGAGATCTCTCTGGTTAGATCACTTT**A**GAAGTCCATTACTTCACCTTGTAAGGAAAGGAAAGAGAAGATTTTTAAGTTTTTTGGTTG	5010
	TGGACTTC**T**AAAGTGAT	5011
	ATCACTTT**A**GAAGTCCA	5012
Male-sterile AG *Lycopersicon esculentum* Arg9Term AGA-TGA	AAAATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCTAACC**T**GAGAGATCTCACCACAAAGGAAACTAGGAAGGGGGAAAATTGAGATCAAAAGGATCGAAA	5013
	TTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAGTTTCCTTTGTGGTGAGATCTCTC**A**GGTTAGATCACTTTGGAAGTCCATTACTTCACCTTGTAAGGAAAGGAAAGAGAAGATTTT	5014
	ATCTAACC**T**GAGAGATC	5015
	GATCTCTC**A**GGTTAGAT	5016
Male-sterile AG *Lycopersicon esculentum* Glu10Term GAG-TAG	ATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCTAACCAGA**T**AGATCTCACCACAAAGGAAACTAGGAAGGGGGAAAATTGAGATCAAAAGGATCGAAAACA	5017
	TGTTTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAGTTTCCTTTGTGGTGAGATCT**A**TCTGGTTAGATCACTTTGGAAGTCCATTACTTCACCTTGTAAGGAAAGGAAAGAGAAGAT	5018
	TAACCAGA**T**AGATCTCA	5019
	TGAGATCT**A**TCTGGTTA	5020
Male-sterile AG *Lycopersicon esculentum* Ser12Term TCA-TGA	CTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCTAACCAGAGAGATCT**G**ACCACAAAGGAAACTAGGAAGGGGGAAAATTGAGATCAAAAGGATCGAAAACACGACGAA	5021
	TTCGTCGTGTTTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAGTTTCCTTTGTGGT**C**AGATCTCTCTGGTTAGATCACTTTGGAAGTCCATTACTTCACCTTGTAAGGAAAGGAAAG	5022
	AGAGATCT**G**ACCACAAA	5023

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTTGTGGTCAGATCTCT	5024
Male-sterile NAG1 *Nicotiana tabacum* Gln4Term CAA-TAA	GTACTCTCTATTTTCATCTTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTCTAAAGTGATCTAACAAGAGAGATCTCTCCACAAAGGAAACTGGGAAGAGGAAAGATTGAGA	5025
	TCTCAATCTTTCCTCTTCCCAGTTTCCTTTGTGGAGAGATCTCTCTTGTTAGATCACTTTAGAAGTCCATACTTTCACCTGGTAAGGAAAGAAAGGGTTGGAAGATGAAAATAGAGAGTAC	5026
	TGGACTTCTAAAGTGAT	5027
	ATCACTTTAGAAGTCCA	5028
Male-sterile NAG1 *Nicotiana tabacum* Arg9Term AGA-TGA	ATCTTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACATGAGAGATCTCTCCACAAAGGAAACTGGGAAGAGGAAAGATTGAGATCAAACGGATCGAAA	5029
	TTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCCAGTTTCCTTTGTGGAGAGATCTCTCATGTTAGATCACTTTGGAAGTCCATACTTTCACCTGGTAAGGAAAGAAAGGGTTGGAAGAT	5030
	ATCTAACATGAGAGATC	5031
	GATCTCTCATGTTAGAT	5032
Male-sterile NAG1 *Nicotiana tabacum* Glu10Term GAG-TAG	TTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACAAGATAGATCTCTCCACAAAGGAAACTGGGAAGAGGAAAGATTGAGATCAAACGGATCGAAAACA	5033
	TGTTTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCCAGTTTCCTTTGTGGAGAGATCTATCTTGTTAGATCACTTTGGAAGTCCATACTTTCACCTGGTAAGGAAAGAAAGGGTTGGAA	5034
	TAACAAGATAGATCTCT	5035
	AGAGATCTATCTTGTTA	5036
Male-sterile NAG1 *Nicotiana tabacum* Gln14Term CAA-TAA	CTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACAAGAGAGATCTCTCCATAAAGGAAACTGGGAAGAGGAAAGATTGAGATCAAACGGATCGAAAACACAACGAATCGTC	5037
	GACGATTCGTTGTGTTTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCCAGTTTCCTTTATGGAGAGATCTCTCTTGTTAGATCACTTTGGAAGTCCATACTTTCACCTGGTAAGGAAAG	5038
	TCTCTCCATAAAGGAAA	5039
	TTTCCTTTATGGAGAGA	5040
Male-sterile AG *Rosa hybrida* Gly22Term GGA-TGA	GCCTATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAGGTGAAAGATCGAGATCAAGCGGATCGAAAACACCACCAATCGTCAAGTCACCTTCTGCAAAA	5041
	TTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTTCGATCCGCTTGATCTCGATCTTTCACCTTCCCAATCTTCTTTGGGCATCAGCGTCCAGGACCGTGTTGGGTTTGTTTTCATAGGC	5042
	TGGGAAGGTGAAAGATC	5043
	GATCTTTCACCTTCCCA	5044

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Rosa hybrida* Lys23Term AAG-TAG	TATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGA AGATTGGGAAGGGGATAGATCGAGATCAAGCGGATCGAAAACAC CACCAATCGTCAAGTCACCTTCTGCAAAAGGC	5045
	GCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTTCGATCC GCTTGATCTCGATCTATCCCCTTCCCAATCTTCTTTGGGCATCAGC GTCCAGGACCGTGTTGGGTTTGTTTTCATA	5046
	GAAGGGGATAGATCGAG	5047
	CTCGATCTATCCCCTTC	5048
Male-sterile AG *Rosa hybrida* Glu25Term GAG-TAG	AACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTG GGAAGGGGAAAGATCTAGATCAAGCGGATCGAAAACACCACCAAT CGTCAAGTCACCTTCTGCAAAAGGCGCAATG	5049
	CATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTT CGATCCGCTTGATCTAGATCTTTCCCCTTCCCAATCTTCTTTGGGC ATCAGCGTCCAGGACCGTGTTGGGTTTGTT	5050
	GAAAGATCTAGATCAAG	5051
	CTTGATCTAGATCTTTC	5052
Male-sterile AG *Rosa hybrida* Lys27 AAG-TAG	CCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAG GGGAAAGATCGAGATCTAGCGGATCGAAAACACCACCAATCGTCA AGTCACCTTCTGCAAAAGGCGCAATGGTTTGC	5053
	GCAAACCATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGG TGTTTTCGATCCGCTAGATCTCGATCTTTCCCCTTCCCAATCTTCT TTGGGCATCAGCGTCCAGGACCGTGTTGGG	5054
	TCGAGATCTAGCGGATC	5055
	GATCCGCTAGATCTCGA	5056
Male-sterile far *Antirrhinum majus* Gln7Term CAA-TAA	CAATTGCCTGTTTTTATTTTTTTTCTTTTTGACTAAGTAGAAATGGC GTCTCTAAGCGATTAATCGACCGAGGTATCGCCCGAGAGGAAAAT CGGGAGAGGAAAGATCGAGATCAAACGGA	5057
	TCCGTTTGATCTCGATCTTTCCTCTCCCGATTTTCCTCTCGGGCGA TACCTCGGTCGATTAATCGCTTAGAGACGCCATTTCTACTTAGTCA AAAAGAAAAAAAATAAAAACAGGCAATTG	5058
	TAAGCGATTAATCGACC	5059
	GGTCGATTAATCGCTTA	5060
Male-sterile far *Antirrhinum majus* Glu10Term GAG-TAG	GTTTTTATTTTTTTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAG CGATCAATCGACCTAGGTATCGCCCGAGAGGAAAATCGGGAGAG GAAAGATCGAGATCAAACGGATCGAAAACA	5061
	TGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTCCCGATTTTCCT CTCGGGCGATACCTAGGTCGATTGATCGCTTAGAGACGCCATTTC TACTTAGTCAAAAAGAAAAAAAATAAAAAC	5062
	AATCGACCTAGGTATCG	5063
	CGATACCTAGGTCGATT	5064

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile far *Antirrhinum majus* Glu14Term GAG-TAG	TTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGA CCGAGGTATCGCCC**T**AGAGGAAAATCGGGAGAGGAAAGATCGAG ATCAAACGGATCGAAAACAAAACAAATCAAC	5065
	GTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTC CCGATTTTCCTCT**A**GGGCGATACCTCGGTCGATTGATCGCTTAGA GACGCCATTTCTACTTAGTCAAAAAGAAA	5066
	TATCGCCC**T**AGAGGAAA	5067
	TTTCCTCT**A**GGGCGATA	5068
Male-sterile far *Antirrhinum majus* Lys16Term AAA-TAA	TTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGACCGAG GTATCGCCCGAGAGG**T**AAATCGGGAGAGGAAAGATCGAGATCAA ACGGATCGAAAACAAAACAAATCAACAGGTTA	5069
	TAACCTGTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTT CCTCTCCCGATTT**A**CCTCTCGGGCGATACCTCGGTCGATTGATCG CTTAGAGACGCCATTTCTACTTAGTCAAA	5070
	CCGAGAGG**T**AAATCGGG	5071
	CCCGATTT**A**CCTCTCGG	5072
Male-sterile AG *Cucumis sativus* Leu21Term TTG-TAG	TGTCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGA AGGAAAGGGTAAGT**A**GCAAATAAAGGGGATGTTCCAGAATCAAGA AGAGAAGATGTCAGACTCGCCTCAGAGGAA	5073
	TTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAACA TCCCCTTTATTTGC**T**ACTTACCCTTTCCTTCTTCCTTAATCATTCTT GTGAGTGGTGACTGATAATGCTTGGACA	5074
	GGGTAAGT**A**GCAAATAA	5075
	TTATTTGC**T**ACTTACCC	5076
Male-sterile AG *Cucumis sativus* Gln22Term CAA-TAA	TCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAG GAAAGGGTAAGTTG**T**AAATAAAGGGGATGTTCCAGAATCAAGAAG AGAAGATGTCAGACTCGCCTCAGAGGAAGA	5077
	TCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAA CATCCCCTTTATTT**A**CAACTTACCCTTTCCTTCTTCCTTAATCATTC TTGTGAGTGGTGACTGATAATGCTTGGA	5078
	GTAAGTTG**T**AAATAAAG	5079
	CTTTATTT**A**CAACTTAC	5080
Male-sterile AG *Cucumis sativus* Lys24Term AAG-TAG	CATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAG GGTAAGTTGCAAATA**T**AGGGGATGTTCCAGAATCAAGAAGAGAAG ATGTCAGACTCGCCTCAGAGGAAGATGGGAA	5081
	TTCCCATCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATT CTGGAACATCCCCT**A**TATTTGCAACTTACCCTTTCCTTCTTCCTTA ATCATTCTTGTGAGTGGTGACTGATAATG	5082
	TGCAAATA**T**AGGGGATG	5083
	CATCCCCT**A**TATTTGCA	5084

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Cucumis sativus* Gln28Term CAG-TAG	CCACTCACAAGAATGATTAAGGAAGAAGGAAAGGGTAAGTTGCAAATAAAGGGGATGTTC**T**AGAATCAAGAAGAGAAGATGTCAGACTCGCCTCAGAGGAAGATGGGAAGAGGAAAGATTG	5085
	CAATCTTTCCTCTTCCCATCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCT**A**GAACATCCCCTTTATTTGCAACTTACCCTTTCCTTCTTCCTTAATCATTCTTGTGAGTGG	5086
	GGATGTTC**T**AGAATCAA	5087
	TTGATTCT**A**GAACATCC	5088
Male-sterile AG *Zea mays* Cys10Term TGC-TGA	CCACCACCACCACCACCACCACCACCACACCATGCTCAACATGATGACTGATCTGAGCTG**A**GGGCCGTCGTCCAAGGTCAAGGAGCAGGTGGCGGCGGCGCCGACGGGCTCCGGCGACAGG	5089
	CCTGTCGCCGGAGCCCGTCGGCGCCGCCGCCACCTGCTCCTTGACCTTGGACGACGGCCC**T**CAGCTCAGATCAGTCATCATGTTGAGCATGGTGTGGTGGTGGTGGTGGTGGTGGTGG	5090
	CTGAGCTG**A**GGGCCGTC	5091
	GACGGCCC**T**CAGCTCAG	5092
Male-sterile AG *Zea mays* Ser13Term TCG-TAG	ACCACCACCACCACCACCACACCATGCTCAACATGATGACTGATCTGAGCTGCGGGCCGT**A**GTCCAAGGTCAAGGAGCAGGTGGCGGCGGCGCCGACGGGCTCCGGCGACAGGCAGGGGCA	5093
	TGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCCGCCGCCACCTGCTCCTTGACCTTGGAC**T**ACGGCCCGCAGCTCAGATCAGTCATCATGTTGAGCATGGTGTGGTGGTGGTGGTGGT	5094
	CGGGCCGT**A**GTCCAAGG	5095
	CCTTGGAC**T**ACGGCCCG	5096
Male-sterile AG *Zea mays* Lys15Term AAG-TAG	CACCACCACCACCACACCATGCTCAACATGATGACTGATCTGAGCTGCGGGCCGTCGTCC**T**AGGTCAAGGAGCAGGTGGCGGCGGCGCCGACGGGCTCCGGCGACAGGCAGGGGCAGGGGA	5097
	TCCCCTGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCCGCCGCCACCTGCTCCTTGACCT**A**GGACGACGGCCCGCAGCTCAGATCAGTCATCATGTTGAGCATGGTGTGGTGGTGGTG	5098
	CGTCGTCC**T**AGGTCAAG	5099
	CTTGACCT**A**GGACGACG	5100
Male-sterile AG *Zea mays* Lys17Term AAG-TAG	CACCACCACACCATGCTCAACATGATGACTGATCTGAGCTGCGGGCCGTCGTCCAAGGTC**T**AGGAGCAGGTGGCGGCGGCGCCGACGGGCTCCGGCGACAGGCAGGGGCAGGGGAGAGGCA	5101
	TGCCTCTCCCCTGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCCGCCGCCACCTGCTCCT**A**GACCTTGGACGACGGCCCGCAGCTCAGATCAGTCATCATGTTGAGCATGGTGTGGTGGTG	5102
	CCAAGGTC**T**AGGAGCAG	5103
	CTGCTCCT**A**GACCTTGG	5104

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Zea mays* Arg4Term CGA-TGA	TCCTACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACA AGAGCATGCACATCTGAGAAGAGGAGGCTACACCATCCACAGTAA CAGGCATCATGTCGACCCTGACTTCGGCGG	5105
	CCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGT GTAGCCTCCTCTTCTCAGATGTGCATGCTCTTGTTCCTATCACACA GATTTTGAGGTCTGAAGGAGAAAAGGTAGGA	5106
	TGCACATCTGAGAAGAG	5107
	CTCTTCTCAGATGTGCA	5108
Male-sterile AG *Zea mays* Glu5Term GAA-TAA	TACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGA GCATGCACATCCGATAAGAGGAGGCTACACCATCCACAGTAACAG GCATCATGTCGACCCTGACTTCGGCGGGGC	5109
	GCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGAT GGTGTAGCCTCCTCTTATCGGATGTGCATGCTCTTGTTCCTATCA CACAGATTTTGAGGTCTGAAGGAGAAAAGGTA	5110
	ACATCCGATAAGAGGAG	5111
	CTCCTCTTATCGGATGT	5112
Male-sterile AG *Zea mays* Glu6Term GAG-TAG	CTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCA TGCACATCCGAGAATAGGAGGCTACACCATCCACAGTAACAGGCA TCATGTCGACCCTGACTTCGGCGGGGCAGC	5113
	GCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTG GATGGTGTAGCCTCCTATTCTCGGATGTGCATGCTCTTGTTCCTA TCACACAGATTTTGAGGTCTGAAGGAGAAAAG	5114
	TCCGAGAATAGGAGGCT	5115
	AGCCTCCTATTCTCGGA	5116
Male-sterile AG *Zea mays* Glu7Term GAG-TAG	TTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATGC ACATCCGAGAAGAGTAGGCTACACCATCCACAGTAACAGGCATCA TGTCGACCCTGACTTCGGCGGGGCAGCAGA	5117
	TCTGCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACT GTGGATGGTGTAGCCTACTCTTCTCGGATGTGCATGCTCTTGTTC CTATCACACAGATTTTGAGGTCTGAAGGAGAA	5118
	GAGAAGAGTAGGCTACA	5119
	TGTAGCCTACTCTTCTC	5120
Male-sterile AG *Oryza sativa* Lys5Term AAG-TAG	GCTGGGTCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGC GAGAAGATGGGGAGGGGGTAGATCGAGATAAAGCGGATCGAGAA CACGACGAACCGGCAGGTGACCTTCTGCAAGCGCC	5121
	GGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCTCGATC CGCTTTATCTCGATCTACCCCCTCCCCATCTTCTCGCTGCTCCCC GCCGCCACCGCCGCCGACGATCCTGACCCAGC	5122
	GGAGGGGGTAGATCGAG	5123
	CTCGATCTACCCCCTCC	5124

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Oryza sativa* Glu7Term GAG-TAG	TCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAGATCTAGATAAAGCGGATCGAGAACACGACGAACCGGCAGGTGACCTTCTGCAAGCGCCGCAATG	5125
	CATTGCGGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCTCGATCCGCTTTATCTAGATCTTCCCCCTCCCCATCTTCTCGCTGCTCCCCGCCGCCACCGCCGCCGACGATCCTGA	5126
	GGAAGATCTAGATAAAG	5127
	CTTTATCTAGATCTTCC	5128
Male-sterile AG *Oryza sativa* Lys9Term AAG-TAG	TCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAGATCGAGATATAGCGGATCGAGAACACGACGAACCGGCAGGTGACCTTCTGCAAGCGCCGCAATGGCCTCC	5129
	GGAGGCCATTGCGGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCTCGATCCGCTATATCTCGATCTTCCCCCTCCCCATCTTCTCGCTGCTCCCCGCCGCCACCGCCGCCGACGA	5130
	TCGAGATATAGCGGATC	5131
	GATCCGCTATATCTCGA	5132
Male-sterile AG *Oryza sativa* Glu12Term GAG-TAG	GCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAGATCGAGATAAAGCGGATCTAGAACACGACGAACCGGCAGGTGACCTTCTGCAAGCGCCGCAATGGCCTCCTGAAGAAGG	5133
	CCTTCTTCAGGAGGCCATTGCGGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCTAGATCCGCTTTATCTCGATCTTCCCCCTCCCCATCTTCTCGCTGCTCCCCGCCGCCACCGC	5134
	AGCGGATCTAGAACACG	5135
	CGTGTTCTAGATCCGCT	5136

Table 16
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Cucumis sativus* Tyr21Term TAT-TAG	GGGAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAGTTACATAGTCAAAGAGAAGAAATGGTATCATCAAAAAAGCCAAAGAAATTACTGTTCTTTGCGATGCT	5137
	AGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCATTTCTTCTCTTTGACTATGTAACTTGTCTATTGCTTGAGTTCTCTATTCTTTTTATTTCTATTTTCCCTCTTCCC	5138

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTACATAGTCAAAGAG	5139
	CTCTTTGACTATGTAAC	5140
Male-sterile PI *Cucumis sativus* Ser22Term TCA-TGA	GAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAGTTACATATTGAAAGAGAAGAAATGGTATCATCAAAAAAGCCAAAGAAATTACTGTTCTTTGCGATGCTCA	5141
	TGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCATTTCTTCTCTTTCAATATGTAACTTGTCTATTGCTTGAGTTCTCTATTCTTTTTATTTCTATTTTCCCTCTTC	5142
	TACATATTGAAAGAGAA	5143
	TTCTCTTTCAATATGTA	5144
Male-sterile PI *Cucumis sativus* Lys23Term AAG-TAG	AGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAGTTACATATTCATAGAGAAGAAATGGTATCATCAAAAAAGCCAAAGAAATTACTGTTCTTTGCGATGCTCAAG	5145
	CTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCATTTCTTCTCTATGAATATGTAACTTGTCTATTGCTTGAGTTCTCTATTCTTTTTATTTCTATTTTCCCTCT	5146
	CATATTCATAGAGAAGA	5147
	TCTTCTCTATGAATATG	5148
Male-sterile PI *Cucumis sativus* Arg24Term AGA-TGA	GGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAGTTACATATTCAAAGTGAAGAAATGGTATCATCAAAAAAGCCAAAGAAATTACTGTTCTTTGCGATGCTCAAGTTT	5149
	AAACTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCATTTCTTCACTTTGAATATGTAACTTGTCTATTGCTTGAGTTCTCTATTCTTTTTATTTCTATTTTCCC	5150
	ATTCAAAGTGAAGAAAT	5151
	ATTTCTTCACTTTGAAT	5152
Male-sterile PI *Malus domestica* Tyr21Term TAC-TAG	GGGACGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGGCAGGTGACCTAGTCCAAGAGGAGGAATGGGATTATCAAGAAGGCAAAGGAGATCACTGTTCTATGTGATGCT	5153
	AGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATCCCATTCCTCCTCTTGGACTAGGTCACCTGCCTGTTACTTGAGTTCTCAATCCTCTTGATCTCAACCTTCCCACGTCCC	5154
	GTGACCTAGTCCAAGAG	5155
	CTCTTGGACTAGGTCAC	5156

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Malus domestica* Lys23Term AAG-TAG	CGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCTAGAGGAGGAATGGGATTATCAAGAAGGCAAAGGAGATCACTGTTCTATGTGATGCTAAAG	5157
	CTTTAGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATCCCATTCCTCCTCTAGGAGTAGGTCACCTGCCTGTTACTTGAGTTCTCAATCCTCTTGATCTCAACCTTCCCACG	5158
	CCTACTCCTAGAGGAGG	5159
	CCTCCTCTAGGAGTAGG	5160
Male-sterile PI *Malus domestica* Lys30Term AAG-TAG	AGGATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGGAGGAATGGGATTATCTAGAAGGCAAAGGAGATCACTGTTCTATGTGATGCTAAAGTATCTCTTATCATTTATTCTA	5161
	TAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGTGATCTCCTTTGCCTTCTAGATAATCCCATTCCTCCTCTTGGAGTAGGTCACCTGCCTGTTACTTGAGTTCTCAATCCT	5162
	GGATTATCTAGAAGGCA	5163
	TGCCTTCTAGATAATCC	5164
Male-sterile PI *Malus domestica* Lys31Term AAG-TAG	ATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGGAGGAATGGGATTATCAAGTAGGCAAAGGAGATCACTGTTCTATGTGATGCTAAAGTATCTCTTATCATTTATTCTAGCT	5165
	AGCTAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGTGATCTCCTTTGCCTACTTGATAATCCCATTCCTCCTCTTGGAGTAGGTCACCTGCCTGTTACTTGAGTTCTCAAT	5166
	TTATCAAGTAGGCAAAG	5167
	CTTTGCCTACTTGATAA	5168
Male-sterile globosa *Antirrhinum majus* Gly2Term GGA-TGA	CATTTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAAAAATGTGAAGAGGAAAAATTGAGATCAAAAGAATTGAGAACTCAAGCAACAGGCAGGTTACTTACT	5169
	AGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATCTCAATTTTTCCTCTTCACATTTTTTTGTTTTTGTTTTTCTCTCTTGTTTTTGTTTGCAGATAACTATTGTAAAAATG	5170
	AAAAAATGTGAAGAGGA	5171
	TCCTCTTCACATTTTTT	5172
Male-sterile globosa *Antirrhinum majus* Arg3Term AGA-TGA	TTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAAAAATGGGATGAGGAAAAATTGAGATCAAAAGAATTGAGAACTCAAGCAACAGGCAGGTTACTTACTCAA	5173
	TTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATCTCAATTTTTCCTCATCCCATTTTTTTGTTTTTGTTTTTCTCTCTTGTTTTTGTTTGCAGATAACTATTGTAAAA	5174

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAATGGGATGAGGAAAA	5175
	TTTTCCTCATCCCATTT	5176
Male-sterile globosa *Antirrhinum majus* Gly4Term GGA-TGA	TACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAAAAATGGGAAGATGAAAAATTGAGATCAAAAGAATTGAGAACTCAAGCAACAGGCAGGTTACTTACTCAAAGA	5177
	TCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATCTCAATTTTTCATCTTCCCATTTTTTTGTTTTTGTTTTTCTCTCTTGTTTTTGTTTGCAGATAACTATTGTA	5178
	TGGGAAGATGAAAAATT	5179
	AATTTTTCATCTTCCCA	5180
Male-sterile globosa *Antirrhinum majus* Lys5Term AAA-TAA	AATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAAAAATGGGAAGAGGATAAATTGAGATCAAAAGAATTGAGAACTCAAGCAACAGGCAGGTTACTTACTCAAAGAGAA	5181
	TTCTCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATCTCAATTTATCCTCTTCCCATTTTTTTGTTTTTGTTTTTCTCTCTTGTTTTTGTTTGCAGATAACTATT	5182
	GAAGAGGATAAATTGAG	5183
	CTCAATTTATCCTCTTC	5184
Male-sterile PI *Zea mays* Lys5Term AAG-TAG	GCTGAGCTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCTAGATCAAGATCAAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCC	5185
	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTTGATCTTGATCTAGCCGCGCCCCATACTGCGTTCTCCACTCCCAAACAGATCCAAGGGCAGCAAGAGCTCAGC	5186
	GGCGCGGCTAGATCAAG	5187
	CTTGATCTAGCCGCGCC	5188
Male-sterile PI *Zea mays* Lys7Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5189
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTGCGTTCTCCACTCCCAAACAGATCCAAGGGCAGCAAGAG	5190
	GCAAGATCTAGATCAAG	5191
	CTTGATCTAGATCTTGC	5192

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Zea mays* Lys9Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5193
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTGCGTTCTCCACTCCCAAACAGATCCAAGGGCAGCAAGAG	5194
	GCAAGATCTAGATCAAG	5195
	CTTGATCTAGATCTTGC	5196
Male-sterile PI *Zea mays* Glu12Term GAG-TAG	GATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGATCAAGATCAAGAGGATCTAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	5197
	CCTTCTTGACCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTAGATCCTCTTGATCTTGATCTTGCCGCGCCCCATACTGCGTTCTCCACTCCCAAACAGATC	5198
	AGAGGATCTAGAACTCT	5199
	AGAGTTCTAGATCCTCT	5200
Male-sterile PI *Zea mays* Lys5Term AAG-TAG	GCTGAGCTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCTAGATCGAGATCAAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCC	5201
	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTTGATCTCGATCTAGCCGCGCCCCATACTCCGTTCTCCACTCCCTAACAGATTCAAGGGCAGCAAGAGCTCAGC	5202
	GGCGCGGCTAGATCGAG	5203
	CTCGATCTAGCCGCGCC	5204
Male-sterile PI *Zea mays* Glu7Term GAG-TAG	CTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5205
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTCCGTTCTCCACTCCCTAACAGATTCAAGGGCAGCAAGAG	5206
	GCAAGATCTAGATCAAG	5207
	CTTGATCTAGATCTTGC	5208
Male-sterile PI *Zea mays* Lys9Term AAG-TAG	CTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGATCGAGATCTAGAGGATCGAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCGGACTGG	5209
	CCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCCTCTAGATCTCGATCTTGCCGCGCCCCATACTCCGTTCTCCACTCCCTAACAGATTCAAGGGCAG	5210

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCGAGATCTAGAGGATC	5211
	GATCCTCTAGATCTCGA	5212
Male-sterile PI *Zea mays* Glu12Term GAG-TAG	AATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGATCGAGATCAAGAGGATCTAGAACTCTACCAACCGGCAGGTGACCTTCTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	5213
	CCTTCTTGACCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTAGATCCTCTTGATCTCGATCTTGCCGCGCCCCATACTCCGTTCTCCACTCCCTAACAGATT	5214
	AGAGGATCTAGAACTCT	5215
	AGAGTTCTAGATCCTCT	5216
Male-sterile PI *Oryza sativa* Lys5Term AAG-TAG	TTGCTGCTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGTAGATCGAGATCAAGAGGATCGAGAACTCCACCAACCGCCAGGTGACCTTCTCCAAGCGCA	5217
	TGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCCTCTTGATCTCGATCTACCCGCGCCCCATCCCGCCTCCTCCTCCTCCTCCTTCCTCCAGCTAGCTTAGCAGCAA	5218
	GGCGCGGGTAGATCGAG	5219
	CTCGATCTACCCGCGCC	5220
Male-sterile PI *Oryza sativa* Glu7Term GAG-TAG	CTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAGATCTAGATCAAGAGGATCGAGAACTCCACCAACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCG	5221
	CGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCCTCTTGATCTAGATCTTCCCGCGCCCCATCCCGCCTCCTCCTCCTCCTCCTCCTTCCTCCAGCTAGCTTAG	5222
	GGAAGATCTAGATCAAG	5223
	CTTGATCTAGATCTTCC	5224
Male-sterile PI *Oryza sativa* Lys9Term AAG-TAG	TAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAGATCGAGATCTAGAGGATCGAGAACTCCACCAACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCGGGATCC	5225
	GGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCCTCTAGATCTCGATCTTCCCGCGCCCCATCCCGCCTCCTCCTCCTCCTCCTCCTTCCTCCAGCTA	5226
	TCGAGATCTAGAGGATC	5227
	GATCCTCTAGATCTCGA	5228

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Oryza sativa* Glu12Term GAG-TAG	GAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAGATCGAGATCAAGAGGATCTAGAACTCCACCAACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCGGGATCCTCAAGAAGG	5229
	CCTTCTTGAGGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTAGATCCTCTTGATCTCGATCTTCCCGCGCCCCATCCCGCCTCCTCCTCCTCCTCCTCCTTC	5230
	AGAGGATCTAGAACTCC	5231
	GGAGTTCTAGATCCTCT	5232

Example 7

Engineering plants for abiotic stress tolerance

Environmental stresses, such as drought, increased soil salinity, soil contamination with heavy metals, and extreme temperature, are major factors limiting plant growth and productivity. The worldwide loss in yield of three major cereal crops, rice, maize, and wheat due to water stress (drought) has been estimated to be over ten billion dollars annually and many currently marginal soils could be brought into cultivation if suitable plant varieties were available.

Physiological and biochemical responses to high levels of ionic or nonionic solutes and decreased water potential have been studied in a variety of plants. It is known, for example, that increasing levels of alcohol dehydrogenase can confer enhances flooding resistance in plants. There are also several possible mechanisms to enhance plant salt tolerance. For example, one mechanism underlying the adaptation or tolerance of plants to osmotic stresses is the accumulation of compatible, low molecular weight osmolytes such as sugar alcohols, special amino acids, and glycinebetaine. Such accumulation can be engineered, for example, by removing feedback inhibition on 1-pyrroline-t-carboxylate synthetase, which results in accumulation of proline. Additionally, recent experiments suggest that altering the expression or activity of specific sodium or potassium transporters can confer enhanced salt tolerance.

Plant tolerance of contamination by heavy metals such as lead and aluminum in soils has also been investigated and one mechanism underlying tolerance is the production of dicarboxylic acids such as oxalate and citrate. In addition, individual genes involved in heavy metal sensitivity have been identified.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer stress tolerance in plants.

Table 17
Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance P5CS *Arabidopsis thaliana* Phe128Ala TTT-GCT	CGTCTTTTTGTGTGGTAGTTGGATGTGACGGTTGCTCAAATGCTT GTGACCGATAGCAGT**GC**TAGAGATAAGGATTTCAGGAAGCAACTT AGTGAAACTGTCAAAGCGATGCTGAGGATGA	5233
	TCATCCTCAGCATCGCTTTGACAGTTTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTA**GC**ACTGCTATCGGTCACAAGCATTTGAGCAACC GTCACATCCAACTACCACACAAAAAGACG	5234
	ATAGCAGT**GC**TAGAGAT	5235
	ATCTCTA**GC**ACTGCTAT	5236
Salt Tolerance P5CS 1 *Brassica napus* Phe128Ala TTC-GCC	GAGACTATGTTTGACCAGCTGGATGTGACGGCTGCTCAGCTGCTG GTGAATGACAGTAGT**GC**CAGAGACAAGGAGTTCAGGAAGCAACTT AATGAGACAGTGAAGTCCATGCTTGATTTGA	5237
	TCAAATCAAGCATGGACTTCACTGTCTCATTAAGTTGCTTCCTGAA CTCCTTGTCTCTG**GC**ACTACTGTCATTCACCAGCAGCTGAGCAGC CGTCACATCCAGCTGGTCAAACATAGTCTC	5238
	ACAGTAGT**GC**CAGAGAC	5239
	GTCTCTG**GC**ACTACTGT	5240
Salt Tolerance P5CS 2 *Brassica napus* Phe129Ala TTC-GCC	GAGACTATGTTTGACCAGATGGATGTGACGGTGGCTCAAATGCTG GTGACTGATAGCAGT**G**TCAGAGATAAGGATTTCAGGAAGCAACTT AGTGAGACAGTCAAAGCTATGCTGAAAATGA	5241
	TCATTTTCAGCATAGCTTTGACTGTCTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTGA**C**ACTGCTATCAGTCACCAGCATTTGAGCCACC GTCACATCCATCTGGTCAAACATAGTCTC	5242
	ATAGCAGT**G**TCAGAGAT	5243
	ATCTCTGA**C**ACTGCTAT	5244
Salt Tolerance P5CS *Oryza sativa* Phe128Ala TTT-GCT	GATATGTTGTTTAACCAACTGGATGTCTCGTCATCTCAACTTCTTG TCACCGACAGTGAT**GC**TGAGAACCCAAAGTTCCGGGAGCAACTCA CTGAAACTGTTGAGTCATTATTAGATCTTA	5245
	TAAGATCTAATAATGACTCAACAGTTTCAGTGAGTTGCTCCCGGAA CTTTGGGTTCTCA**GC**ATCACTGTCGGTGACAAGAAGTTGAGATGA CGAGACATCCAGTTGGTTAAACAACATATC	5246
	ACAGTGAT**GC**TGAGAAC	5247
	GTTCTCA**GC**ATCACTGT	5248

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance P5CS *Medicago sativa* Phe128Ala TTT-GCT	GATATTTTGTTTAGTCAGCTGGATGTGACATCTGCTCAGCTTCTTG TTACTGACAATGAT**GC**TAGAGACCAAGATTTTAGAAAGCAACTTTC TGAAACTGTGAGATCACTTCTAGCACTAA	5249
	TTAGTGCTAGAAGTGATCTCACAGTTTCAGAAAGTTGCTTTCTAAA ATCTTGGTCTCTA**GC**ATCATTGTCAGTAACAAGAAGCTGAGCAGAT GTCACATCCAGCTGACTAAACAAAATATC	5250
	ACAATGAT**GC**TAGAGAC	5251
	GTCTCTA**GC**ATCATTGT	5252
Salt Tolerance P5CS *Actinidia deliciosa* Phe128Ala TTT-GCT	GATACATTGTTTAGTCAGCTGGATGTGACATCAGCTCAGCTACTC GTTACTGATAATGAT**GC**TAGGGATCCAGAATTCAGGAAGCAACTTA CTGAAACTGTAGAATCACTATTGAATTTGA	5253
	TCAAATTCAATAGTGATTCTACAGTTTCAGTAAGTTGCTTCCTGAAT TCTGGATCCCTA**GC**ATCATTATCAGTAACGAGTAGCTGAGCTGAT GTCACATCCAGCTGACTAAACAATGTATC	5254
	ATAATGAT**GC**TAGGGAT	5255
	ATCCCTA**GC**ATCATTAT	5256
Salt Tolerance P5CS *Cichorium intybus* Phe122Ala TTC-GCC	GACACACTCTTCAGTCAACTGGATGTGACATCAGCACAGCTTCTT GTAACAGATAATGAC**GC**CAGAAGTCCAGAATTTAGAAAACAACTTA CTGAAACAGTCGATTCTTTATTATCTTATA	5257
	TATAAGATAATAAAGAATCGACTGTTTCAGTAAGTTGTTTTCTAAAT TCTGGACTTCTG**GC**GTCATTATCTGTTACAAGAAGCTGTGCTGAT GTCACATCCAGTTGACTGAAGAGTGTGTC	5258
	ATAATGAC**GC**CAGAAGT	5259
	ACTTCTG**GC**GTCATTAT	5260
Salt Tolerance P5CS *Lycopersicon esculentum* Phe128Ala TTT-GCT	GATTCTTTGTTCAGTCAGTTGGATGTGACATCAGCTCAGCTTCTGG TGACTGATAATGAC**GC**TAGAGATCCAGATTTTAGGAGACAACTCAA TGACACAGTAAATTCGTTGCTTTCTCTAA	5261
	TTAGAGAAAGCAACGAATTTACTGTGTCATTGAGTTGTCTCCTAAA ATCTGGATCTCTA**GC**GTCATTATCAGTCACCAGAAGCTGAGCTGA TGTCACATCCAACTGACTGAACAAAGAATC	5262
	ATAATGAC**GC**TAGAGAT	5263
	ATCTCTA**GC**GTCATTAT	5264
Salt Tolerance P5CS *Vigna unguiculata* Phe162Ala TTT-GCT	GATACCATGTTCAGCCAGCTTGATGTGACTTCTTCCCAACTTCTTG TGAATGATGGATTT**GC**TAGGGATGCTGGCTTCAGAAAACAACTTTC GGACACAGTGAACGCGTTATTAGATTTAA	5265
	TTAAATCTAATAACGCGTTCACTGTGTCCGAAAGTTGTTTTCTGAA GCCAGCATCCCTA**GC**AAATCCATCATTCACAAGAAGTTGGGAAGA AGTCACATCAAGCTGGCTGAACATGGTATC	5266
	ATGGATTT**GC**TAGGGAT	5267

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATCCCTA**GC**AAATCCAT	5268
Salt Tolerance P5CS *Mesembryanthemum crystallinum* Phe125Ala TTT-GCT	GACACCTTGTTTAGTCAGTTGGATCTGACTGCTGCTCAGCTGCTTGTGACGGACAACGAC**GC**TAGAGATCCAAGTTTTAGAACACAACTAACTGAAACAGTGTATCAGTTGTTGGATCTAA	5269
	TTAGATCCAACAACTGATACACTGTTTCAGTTAGTTGTGTTCTAAAACTTGGATCTCTA**GC**GTCGTTGTCCGTCACAAGCAGCTGAGCAGCAGTCAGATCCAACTGACTAAACAAGGTGTC	5270
	ACAACGAC**GC**TAGAGAT	5271
	ATCTCTA**GC**GTCGTTGT	5272
Salt Tolerance P5CS *Vitis vinifera* Phe130Ala TTT-GCT	GACACATTATTTAGCCAGCTGGATGTGACATCAGCTCAGCTTCTTGTGACTGATAATGAT**GC**TAGGGATGAAGCTTTCCGAAATCAACTTACTCAAACAGTGGATTCATTGTTAGCTTTGA	5273
	TCAAAGCTAACAATGAATCCACTGTTTGAGTAAGTTGATTTCGGAAAGCTTCATCCCTA**GC**ATCATTATCAGTCACAAGAAGCTGAGCTGATGTCACATCCAGCTGGCTAAATAATGTGTC	5274
	ATAATGAT**GC**TAGGGAT	5275
	ATCCCTA**GC**ATCATTAT	5276
Salt Tolerance P5CS *Vigna aconitifolia* Phe129Ala TTT-GCT	GATACGCTGTTCACTCAGCTCGATGTGACATCGGCTCAGCTTCTTGTGACGGATAACGAT**GC**TCGAGATAAGGATTTCAGGAAGCAGCTTACTGAGACTGTGAAGTCGCTGTTGGCGCTGA	5277
	TCAGCGCCAACAGCGACTTCACAGTCTCAGTAAGCTGCTTCCTGAAATCCTTATCTCGA**GC**ATCGTTATCCGTCACAAGAAGCTGAGCCGATGTCACATCGAGCTGAGTGAACAGCGTATC	5278
	ATAACGAT**GC**TCGAGAT	5279
	ATCTCGA**GC**ATCGTTAT	5280
Salt Tolerance HKT1 *Arabidopsis thaliana* Ser207Val TCC-GTC	AGAGATGTTCTTAGTTCCAAAGAAATCTCACCTCTCACTTTCTCCGTCTTCACAACAGTT**GT**CACGTTTGCAAACTGCGGATTTGTCCCCACGAATGAGAACATGATCATCTTTCGCAAAA	5281
	TTTTGCGAAAGATGATCATGTTCTCATTCGTGGGGACAAATCCGCAGTTTGCAAACGTG**AC**AACTGTTGTGAAGACGGAGAAAGTGAGAGGTGAGATTTCTTTGGAACTAAGAACATCTCT	5282
	CAACAGTT**GT**CACGTTT	5283
	AAACGTG**AC**AACTGTTG	5284
Salt Tolerance HKT1 *Arabidopsis thaliana* Gln237Leu CAA-CTA	CGAATGAGAACATGATCATCTTTCGCAAAAACTCTGGTCTCATCTGGCTCCTAATCCCTC**T**AGTACTGATGGGAAACACTTTGTTCCCTTGCTTCTTGGTTTTGCTCATATGGGGACTTTA	5285
	TAAAGTCCCCATATGAGCAAAACCAAGAAGCAAGGGAACAAAGTGTTTCCCATCAGTACT**A**GAGGGATTAGGAGCCAGATGAGACCAGAGTTTTTGCGAAAGATGATCATGTTCTCATTCG	5286

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCCCTC**T**AGTACTGA	5287
	TCAGTACT**A**GAGGGATT	5288
Salt Tolerance HKT1 *Arabidopsis thaliana* Asn332Ser AAT-AGT	AGTCTCTAGAAGGAATGAGTTCGTACGAGAAGTTGGTTGGATCGT TGTTTCAAGTGGTGA**G**TTCGCGACACACCGGAGAAACTATAGTAG ACCTCTCTACACTTTCCCCAGCTATCTTGGT	5289
	ACCAAGATAGCTGGGGAAAGTGTAGAGAGGTCTACTATAGTTTCT CCGGTGTGTCGCGAA**C**TCACCACTTGAAACAACGATCCAACCAAC TTCTCGTACGAACTCATTCCTTCTAGAGACT	5290
	AGTGGTGA**G**TTCGCGAC	5291
	GTCGCGAA**C**TCACCACT	5292
Salt Tolerance HKT1 *Eucalyptus camaldulensis* Ser256Val TCG-GTG	AGAGATGTGCTAAAGAAGAAAGGTCTCAAAATGGTGACCTTTTCC GTCTTCACCACCGTG**GT**GACCTTTGCCAGTTGTGGGTTTGTCCCG ACCAATGAAAACATGATTATCTTCAGCAAAA	5293
	TTTTGCTGAAGATAATCATGTTTTCATTGGTCGGGACAAACCCACA ACTGGCAAAGGTC**AC**CACGGTGGTGAAGACGGAAAAGGTCACCA TTTTGAGACCTTTCTTCTTTAGCACATCTCT	5294
	CCACCGTG**GT**GACCTTT	5295
	AAAGGTC**AC**CACGGTGG	5296
Salt Tolerance HKT1 *Eucalyptus camaldulensis* Gln286Leu CAG-CTG	CCAATGAAAACATGATTATCTTCAGCAAAAACTCTGGCCTCCTCCT GATTCTCATCCCTC**T**GGCCCTTCTTGGGAACATGCTGTTCCCATC GAGCCTACGTTTGACGCTTTGGCTCATCGG	5297
	CCGATGAGCCAAAGCGTCAAACGTAGGCTCGATGGGAACAGCAT GTTCCCAAGAAGGGCC**A**GAGGGATGAGAATCAGGAGGAGGCCA GAGTTTTTGCTGAAGATAATCATGTTTTCATTGG	5298
	CATCCCTC**T**GGCCCTTC	5299
	GAAGGGCC**A**GAGGGATG	5300
Salt Tolerance HKT1 *Eucalyptus camaldulensis* Asn381Ser AAC-AGC	AATCGTTGAATGGACTAAGCTCCTGTGAGAAAATCGTGGGCGCGC TGTTTCAGTGCGTGA**G**CAGCAGACATACCGGCGAGACGGTCGTC GATCTGTCCACAGTTGCTCCCGCCATCTTGGT	5301
	ACCAAGATGGCGGGAGCAACTGTGGACAGATCGACGACCGTCTC GCCGGTATGTCTGCTG**C**TCACGCACTGAAACAGCGCGCCCACGA TTTTCTCACAGGAGCTTAGTCCATTCAACGATT	5302
	GTGCGTGA**G**CAGCAGAC	5303
	GTCTGCTG**C**TCACGCAC	5304

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance HKT1 *Oryza sativa* Ser238Val TCC-GTC	AAAGCTCCACTGAAGAAGAAAGGGATCAACATTGCACTCTTCTCATTCTCGGTCACGGTC**GT**CTCGTTTGCGAATGTGGGGCTCGTGCCGACAAATGAGAACATGGCAATCTTCTCCAAGA	5305
	TCTTGGAGAAGATTGCCATGTTCTCATTTGTCGGCACGAGCCCCACATTCGCAAACGAG**AC**GACCGTGACCGAGAATGAGAAGAGTGCAATGTTGATCCCTTTCTTCTTCAGTGGAGCTTT	5306
	TCACGGTC**GT**CTCGTTT	5307
	AAACGAG**AC**GACCGTGA	5308
Salt Tolerance HKT1 *Oryza sativa* Gln268Leu CAG-CTG	CAAATGAGAACATGGCAATCTTCTCCAAGAACCCGGGCCTCCTCCTCCTGTTCATCGGCC**T**GATTCTTGCAGGCAATACACTTTACCCTCTCTTCCTAAGGCTATTGATATGGTTCCTGGG	5309
	CCCAGGAACCATATCAATAGCCTTAGGAAGAGAGGGTAAAGTGTATTGCCTGCAAGAATC**A**GGCCGATGAACAGGAGGAGGAGGCCCGGGTTCTTGGAGAAGATTGCCATGTTCTCATTTG	5310
	CATCGGCC**T**GATTCTTG	5311
	CAAGAATC**A**GGCCGATG	5312
Salt Tolerance HKT1 *Oryza sativa* Asn363Ser AAC-AGC	CAGTCTTTGATGGACTCAGCTCTTACCAGAAGATTATCAATGCATTGTTCATGGCAGTGA**G**CGCAAGGCACTCGGGGGAGAACTCCATCGACTGCTCACTCATCGCCCCTGCTGTTCTAGT	5313
	ACTAGAACAGCAGGGGCGATGAGTGAGCAGTCGATGGAGTTCTCCCCCGAGTGCCTTGCG**C**TCACTGCCATGAACAATGCATTGATAATCTTCTGGTAAGAGCTGAGTCCATCAAAGACTG	5314
	GGCAGTGA**G**CGCAAGGC	5315
	GCCTTGCG**C**TCACTGCC	5316
Salt Tolerance HKT1 *Triticum aestivum* Ala240Val GCC-GTC	GTGCCCCACTGAACAAGAAAGGGATCAACATCGTGCTCTTCTCACTATCAGTCACCGTTG**T**CTCCTGTGCGAATGCAGGACTCGTGCCCACAAATGAGAACATGGTCATCTTCTCAAAGAA	5317
	TTCTTTGAGAAGATGACCATGTTCTCATTTGTGGGCACGAGTCCTGCATTCGCACAGGAG**A**CAACGGTGACTGATAGTGAGAAGAGCACGATGTTGATCCCTTTCTTGTTCAGTGGGGCAC	5318
	CACCGTTG**T**CTCCTGTG	5319
	CACAGGAG**A**CAACGGTG	5320
Salt Tolerance HKT1 *Triticum aestivum* Gln270Leu CAG-CTG	CAAATGAGAACATGGTCATCTTCTCAAAGAATTCAGGCCTCTTGTTGCTGCTGAGTGGCC**T**GATGCTCGCAGGCAATACATTGTTCCCTCTCTTCCTGAGGCTACTGGTGTGGTTCCTGGG	5321
	CCCAGGAACCACACCAGTAGCCTCAGGAAGAGAGGGAACAATGTATTGCCTGCGAGCATC**A**GGCCACTCAGCAGCAACAAGAGGCCTGAATTCTTTGAGAAGATGACCATGTTCTCATTTG	5322
	GAGTGGCC**T**GATGCTCG	5323

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGAGCATC**A**GGCCACTC	5324
Salt Tolerance HKT1 *Triticum aestivum* Asn365Ser AAT-AGT	CAGTCTTTGATGGGCTCAGCTCTTATCAGAAGACTGTCAATGCATTCTTCATGGTGGTGA**G**TGCGAGGCACTCAGGGGAGAATTCCATCGACTGCTCGCTCATGTCCCCTGCCATTATAGT	5325
	ACTATAATGGCAGGGGACATGAGCGAGCAGTCGATGGAATTCTCCCCTGAGTGCCTCGCA**C**TCACCACCATGAAGAATGCATTGACAGTCTTCTGATAAGAGCTGAGCCCATCAAAGACTG	5326
	GGTGGTGA**G**TGCGAGGC	5327
	GCCTCGCA**C**TCACCACC	5328
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Arg7Term CGA-TGA	TTTTTTTTGTTTTCGTTTTCAAAAACAAAATCTTTGAATTTTATGGCAACCCGTCTTCTC**T**GAACAAACTTTATCCGGCGATCTTACCGTTTACCCGCTTTTAGCCCGGTGGGTCCTCCCA	5329
	TGGGAGGACCCACCGGGCTAAAAGCGGGTAAACGGTAAGATCGCCGGATAAAGTTTGTTC**A**GAGAAGACGGGTTGCCATAAAATTCAAAGATTTTGTTTTTGAAAACGAAAACAAAAAAAA	5330
	GTCTTCTC**T**GAACAAAC	5331
	GTTTGTTC**A**GAGAAGAC	5332
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Arg13Term CGA-TGA	TCAAAAACAAAATCTTTGAATTTTATGGCAACCCGTCTTCTCAGAACAAACTTTATCCGG**T**GATCTTACCGTTTACCCGCTTTTAGCCCGGTGGGTCCTCCCACCGTGACTGCTTCCACCG	5333
	CGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAAGCGGGTAAACGGTAAGATC**A**CCGGATAAAGTTTGTTCTGAGAAGACGGGTTGCCATAAAATTCAAAGATTTTGTTTTTGA	5334
	TTATCCGG**T**GATCTTAC	5335
	GTAAGATC**A**CCGGATAA	5336
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Tyr15Term TAC-TAG	AAAATCTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAAACTTTATCCGGCGATCTTA**G**CGTTTACCCGCTTTTAGCCCGGTGGGTCCTCCCACCGTGACTGCTTCCACCGCCGTCGTC	5337
	GACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAAGCGGGTAAACG**C**TAAGATCGCCGGATAAAGTTTGTTCGGAGAAGACGGGTTGCCATAAAATTCAAAGATTTT	5338
	CGATCTTA**G**CGTTTACC	5339
	GGTAAACG**C**TAAGATCG	5340

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Leu17Term TTA-TAA	CTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAAACTTTATCCGGCGATCTTACCGTT**A**ACCCGCTTTTAGCCCGGTGGGTCCTCCCACCGTGACTGCTTCCACCGCCGTCGTCCCGGA	5341
	TCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAAGCGGGT**T**AACGGTAAGATCGCCGGATAAAGTTTGTTCGGAGAAGACGGGTTGCCATAAAATTCAAAG	5342
	TTACCGTT**A**ACCCGCTT	5343
	AAGCGGGT**T**AACGGTAA	5344
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Gly42Term GGA-TGA	CCGGTGGGTCCTCCCACCGTGACTGCTTCCACCGCCGTCGTCCCGGAGATTCTCTCCTTT**T**GACAACAAGCACCGGAACCACCTCTTCACCACCCAAAACCCACCGAGCAATCTCACGATG	5345
	CATCGTGAGATTGCTCGGTGGGTTTTGGGTGGTGAAGAGGTGGTTCCGGTGCTTGTTGTC**A**AAAGGAGAGAATCTCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGG	5346
	TCTCCTTT**T**GACAACAA	5347
	TTGTTGTC**A**AAAGGAGA	5348
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Arg4Term CGA-TGA	ACATGAAGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACTATGAATTTC**T**GACAAGAGAAGTTTGTAAGGTCAGTGTTCCAGATTTGTCTCATTGAATTCTAAGTCGTGA	5349
	TCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTACAAACTTCTCTTGTC**A**GAAATTCATAGTTTGAGACTAATAAGATTCAATACAAACAGAGATTTCACTGCTTCATGT	5350
	TGAATTTC**T**GACAAGAG	5351
	CTCTTGTC**A**GAAATTCA	5352
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Gln5Term CAA-TAA	TGAAGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACTATGAATTTCCGA**T**AAGAGAAGTTTGTAAGGTCAGTGTTCCAGATTTGTCTCATTGAATTCTAAGTCGTGAAGC	5353
	GCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTACAAACTTCTCTT**A**TCGGAAATTCATAGTTTGAGACTAATAAGATTCAATACAAACAGAGATTTCACTGCTTCA	5354
	ATTTCCGA**T**AAGAGAAG	5355
	CTTCTCTT**A**TCGGAAAT	5356
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Glu6Term GAG-TAG	AGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACTATGAATTTCCGACAA**T**AGAAGTTTGTAAGGTCAGTGTTCCAGATTTGTCTCATTGAATTCTAAGTCGTGAAGCTTA	5357
	TAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTACAAACTTCT**A**TTGTCGGAAATTCATAGTTTGAGACTAATAAGATTCAATACAAACAGAGATTTCACTGCT	5358

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACAATAGAAGTTT	5359
	AAACTTCTATTGTCGGA	5360
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Lys7Term AAG-TAG	AGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACTATGAATTTCCGACAAGAGTAGTTTGTAAGGTCAGTGTTCCAGATTTGTCTCATTGAATTCTAAGTCGTGAAGCTTAATT	5361
	AATTAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTACAAACTACTCTTGTCGGAAATTCATAGTTTGAGACTAATAAGATTCAATACAAACAGAGATTTCACT	5362
	GACAAGAGTAGTTTGTA	5363
	TACAAACTACTCTTGTC	5364
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Gln12Term CAA-TAA	CATTGAATTCTAAGTCGTGAAGCTTAATTCGATTCTTCTTCACTTTCTCGGATCAGGTTTTAAGATTGGAAGTCGGATAAGACTTCCTCCGACGTGGAATATTCCGGTAAAAACGAGATTC	5365
	GAATCTCGTTTTTACCGGAATATTCCACGTCGGAGGAAGTCTTATCCGACTTCCAATCTTAAAACCTGATCCGAGAAAGTGAAGAAGAATCGAATTAAGCTTCACGACTTAGAATTCAATG	5366
	TCAGGTTTTAAGATTGG	5367
	CCAATCTTAAAACCTGA	5368
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gln5Term CAA-TAA	TGGAAGTCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCTAAGACGAGTTTGTGAGGTTTCAGGATTGGAAATCAGAGAGAAGCTCTGAGGGAAATTTTC	5369
	GAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCTGAAACCTCACAAACTCGTCTTAGCGGTGATTCATAACTTTAGCCAATGCATCAACCTGCTCAACGTGGGGGATTGACTTCCA	5370
	ATCACCGCTAAGACGAG	5371
	CTCGTCTTAGCGGTGAT	5372
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gly7Term GAG-TAG	TCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACTAGTTTGTGAGGTTTCAGGATTGGAAATCAGAGAGAAGCTCTGAGGGAAATTTTCATGCTA	5373
	TAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCTGAAACCTCACAAACTAGTCTTGGCGGTGATTCATAACTTTAGCCAATGCATCAACCTGCTCAACGTGGGGGATTGA	5374
	GCCAAGACTAGTTTGTG	5375
	CACAAACTAGTCTTGGC	5376

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gln12Term CAG-TAG	GAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTGAGGTTT**T**AGGATTGGAAATCAGAGAGAAGCTCTGAGGGAAATTTTCATGCTAAAGGTGGAGTCCACC	5377
	GGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCT**A**AAACCTCACAAACTCGTCTTGGCGGTGATTCATAACTTTAGCCAATGCATCAACCTGCTC	5378
	TGAGGTTT**T**AGGATTGG	5379
	CCAATCCT**A**AAACCTCA	5380
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Trp14Term TGG-TGA	TGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTGAGGTTTCAGGATTG**T**AAATCAGAGAGAAGCTCTGAGGGAAATTTTCATGCTAAAGGTGGAGTCCACCGAAGTAAA	5381
	TTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTT**A**CAATCCTGAAACCTCACAAACTCGTCTTGGCGGTGATTCATAACTTTAGCCAATGCATCA	5382
	CAGGATTG**T**AAATCAGA	5383
	TCTGATTT**A**CAATCCTG	5384
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Lys15Term AAA-TAA	GATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTGAGGTTTCAGGATTGG**T**AATCAGAGAGAAGCTCTGAGGGAAATTTTCATGCTAAAGGTGGAGTCCACCGAAGTAAAG	5385
	CTTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATT**A**CCAATCCTGAAACCTCACAAACTCGTCTTGGCGGTGATTCATAACTTTAGCCAATGCATC	5386
	AGGATTGG**T**AATCAGAG	5387
	CTCTGATT**A**CCAATCCT	5388
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Glu2Term GAA-TAA	CTTGAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAGATAATGATG**T**AAAGAGAGGACAGATATGTTAGATTTCAGGACTGCAAATCAGAGCAATCTGTTATCTCAG	5389
	CTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAACATATCTGTCCTCTCTTT**A**CATCATTATCTCCACCAGGCGAACAGTTAGCAGCTAAGAGTGGTAGATCAATTCTTCAAG	5390
	TAATGATG**T**AAAGAGAG	5391
	CTCTCTTT**A**CATCATTA	5392

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Arg3Term AGA-TGA	GAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTG GAGATAATGATGGAATGAGAGGACAGATATGTTAGATTTCAGGAC TGCAAATCAGAGCAATCTGTTATCTCAGAGA	5393
	TCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAAC ATATCTGTCCTCTCATTCCATCATTATCTCCACCAGGCGAACAGTT AGCAGCTAAGAGTGGTAGATCAATTCTTC	5394
	TGATGGAATGAGAGGAC	5395
	GTCCTCTCATTCCATCA	5396
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Glu4Term GAG-TAG	GAATTGATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAG ATAATGATGGAAAGATAGGACAGATATGTTAGATTTCAGGACTGCA AATCAGAGCAATCTGTTATCTCAGAGAACG	5397
	CGTTCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCT AACATATCTGTCCTATCTTTCCATCATTATCTCCACCAGGCGAACA GTTAGCAGCTAAGAGTGGTAGATCAATTC	5398
	TGGAAAGATAGGACAGA	5399
	TCTGTCCTATCTTTCCA	5400
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Arg6Term AGA-TGA	ATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAGATAATG ATGGAAAGAGAGGACTGATATGTTAGATTTCAGGACTGCAAATCA GAGCAATCTGTTATCTCAGAGAACGCAGTTT	5401
	AAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTG AAATCTAACATATCAGTCCTCTCTTTCCATCATTATCTCCACCAGG CGAACAGTTAGCAGCTAAGAGTGGTAGAT	5402
	GAGAGGACTGATATGTT	5403
	AACATATCAGTCCTCTC	5404
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Tyr7Term TAT-TAG	CCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAGATAATGATGGA AAGAGAGGACAGATAGGTTAGATTTCAGGACTGCAAATCAGAGCA ATCTGTTATCTCAGAGAACGCAGTTTCACCA	5405
	TGGTGAAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTTGCAG TCCTGAAATCTAACCTATCTGTCCTCTCTTTCCATCATTATCTCCAC CAGGCGAACAGTTAGCAGCTAAGAGTGG	5406
	GACAGATAGGTTAGATT	5407
	AATCTAACCTATCTGTC	5408
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Glu2Term GAG-TAG	ATCCTTCTCTGAGAAAAAACAACAGATCCGAATTTTATCTTTAATCA GCCGGAAAAAATGTAGAAAGCGATCGAGAGACAACGCGTTCTTCT TGAGCATCTCCGACCTTCTTCTTCTTCTT	5409
	AAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTTGTC TCTCGATCGCTTTCTACATTTTTTCCGGCTGATTAAAGATAAAATTC GGATCTGTTGTTTTTTCTCAGAGAAGGAT	5410

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAAATGTAGAAAGCG	5411
	CGCTTTCTACATTTTTT	5412
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Lys3Term AAA-TAA	CTTCTCTGAGAAAAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGTAAGCGATCGAGAGACAACGCGTTCTTCTTGAGCATCTCCGACCTTCTTCTTCTTCTTCGC	5413
	GCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTTGTCTCTCGATCGCTTACTCCATTTTTTCCGGCTGATTAAAGATAAAATTCGGATCTGTTGTTTTTTCTCAGAGAAG	5414
	AAATGGAGTAAGCGATC	5415
	GATCGCTTACTCCATTT	5416
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Glu6Term GAG-TAG	GAAAAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGAAAGCGATCTAGAGACAACGCGTTCTTCTTGAGCATCTCCGACCTTCTTCTTCTTCTTCGCACAATTACG	5417
	CGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTTGTCTCTAGATCGCTTTCTCCATTTTTTCCGGCTGATTAAAGATAAAATTCGGATCTGTTGTTTTTTC	5418
	AAGCGATCTAGAGACAA	5419
	TTGTCTCTAGATCGCTT	5420
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Arg7Term AGA-TGA	AAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGAAAGCGATCGAGTGACAACGCGTTCTTCTTGAGCATCTCCGACCTTCTTCTTCTTCTTCGCACAATTACGAGG	5421
	CCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTTGTCACTCGATCGCTTTCTCCATTTTTTCCGGCTGATTAAAGATAAAATTCGGATCTGTTGTTTT	5422
	CGATCGAGTGACAACGC	5423
	GCGTTGTCACTCGATCG	5424
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Gln8Term CAA-TAA	ACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGAAAGCGATCGAGAGATAACGCGTTCTTCTTGAGCATCTCCGACCTTCTTCTTCTTCTTCGCACAATTACGAGGCTT	5425
	AAGCCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTTATCTCTCGATCGCTTTCTCCATTTTTTCCGGCTGATTAAAGATAAAATTCGGATCTGTTGT	5426
	TCGAGAGATAACGCGTT	5427
	AACGCGTTATCTCTCGA	5428

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Glu26Term GAA-TAA	GAGAGACAAAGAGTTCTTCTTGAACATCTCCGTCCTTCTTCTTCTTCCTCTCACAGCTTT**T**AAGGCTCTCTCTCTGCTTCAGCTTGCTTGGCTGGGGACAGTGCTGCGTATCAGAGGACCT	5429
	AGGTCCTCTGATACGCAGCACTGTCCCCAGCCAAGCAAGCTGAAGCAGAGAGAGAGCCTT**A**AAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGATGTTCAAGAAGAACTCTTTGTCTCTC	5430
	ACAGCTTT**T**AAGGCTCT	5431
	AGAGCCTT**A**AAAGCTGT	5432
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Ser32Term TCA-TGA	TTGAACATCTCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGGCTCTCTCTCTGCTT**G**AGCTTGCTTGGCTGGGGACAGTGCTGCGTATCAGAGGACCTCTCTCTATGGAGATGATGT	5433
	ACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGCACTGTCCCCAGCCAAGCAAGCT**C**AAGCAGAGAGAGAGCCTTCAAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGATGTTCAA	5434
	CTCTGCTT**G**AGCTTGCT	5435
	AGCAAGCT**C**AAGCAGAG	5436
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Cys34Term TGC-TGA	TCTCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGGCTCTCTCTCTGCTTCAGCTTG**A**TTGGCTGGGGACAGTGCTGCGTATCAGAGGACCTCTCTCTATGGAGATGATGTAGTCATT	5437
	AATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGCACTGTCCCCAGCCAA**T**CAAGCTGAAGCAGAGAGAGAGCCTTCAAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5438
	TCAGCTTG**A**TTGGCTGG	5439
	CCAGCCAA**T**CAAGCTGA	5440
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Leu35Term TTG-TAG	TCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGGCTCTCTCTCTGCTTCAGCTTGCT**A**GGCTGGGGACAGTGCTGCGTATCAGAGGACCTCTCTCTATGGAGATGATGTAGTCATTGT	5441
	ACAATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGCACTGTCCCCAGCC**T**AGCAAGCTGAAGCAGAGAGAGAGCCTTCAAAGCTGTGAGAGGAAGAAGAAGAAGGACGGA	5442
	AGCTTGCT**A**GGCTGGGG	5443
	CCCCAGCC**T**AGCAAGCT	5444

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Tyr42Term TAT-TAG	TCACAGCTTTGAAGGCTCTCTCTCTGCTTCAGCTTGCTTGGCTGGGGACAGTGCTGCGTA**G**CAGAGGACCTCTCTCTATGGAGATGATGTAGTCATTGTTGCGGCACATAGGACTGCACTA	5445
	TAGTGCAGTCCTATGTGCCGCAACAATGACTACATCATCTCCATAGAGAGAGGTCCTCTG**C**TACGCAGCACTGTCCCCAGCCAAGCAAGCTGAAGCAGAGAGAGAGAGCCTTCAAAGCTGTGA	5446
	GCTGCGTA**G**CAGAGGAC	5447
	GTCCTCTG**C**TACGCAGC	5448
2,4-DB resistance 3-ketoacyl-CoA thiolase B *Mangifera indica* Tyr25Term TAC-TAG	CAACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTCTTCTTCTCACAATTA**G**GAGTCCGCTCTTGCCGCATCAGTATGTGCTGCAGGGGATAGCGCCGCATATCATAGGGCT	5449
	AGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATGCGGCAAGAGCGGACTC**C**TAATTGTGAGAAGAAGAATTAGAAGGGCGGAGATGCTGGAGCAACACTTGCTGTCTGTTG	5450
	CACAATTA**G**GAGTCCGC	5451
	GCGGACTC**C**TAATTGTG	5452
2,4-DB resistance 3-ketoacyol-CoA thiolase B *Magnifera indica* Glu26Term GAG-TAG	AACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTCTTCTTCTCACAATTAC**T**AGTCCGCTCTTGCCGCATCAGTATGTGCTGCAGGGGATAGCGCCGCATATCATAGGGCTT	5453
	AAGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATGCGGCAAGAGCGGACT**A**GTAATTGTGAGAAGAAGAATTAGAAGGGCGGAGATGCTGGAGCAACACTTGCTGTCTGTT	5454
	ACAATTAC**T**AGTCCGCT	5455
	AGCGGACT**A**GTAATTGT	5456
2,4-DB resistance 3-ketoacylol-CoA thiolase B *Mangifera indica* Ser32Term TCA-TGA	TCCAGCATCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTCCGCTCTTGCCGCAT**G**AGTATGTGCTGCAGGGGATAGCGCCGCATATCATAGGGCTTCTGTTTATGGAGACGATGT	5457
	ACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACT**C**ATGCGGCAAGAGCGGACTCGTAATTGTGAGAAGAAGAATTAGAAGGGCGGAGATGCTGGA	5458
	TGCCGCAT**G**AGTATGTG	5459
	CACATACT**C**ATGCGGCA	5460

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase B *Mangifera indica* Cys34Term TGT-TGA	TCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTCCGCTCTTGCCGCATCAGTATG**A**GCTGCAGGGGATAGCGCCGCATATCATAGGGCTTCTGTTTATGGAGACGATGTGGTGATT	5461
	AATCACCACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGCGCTATCCCCTGCAGC**T**CATACTGATGCGGCAAGAGCGGACTCGTAATTGTGAGAAGAAGAATTAGAAGGGCGGAGA	5462
	TCAGTATG**A**GCTGCAGG	5463
	CCTGCAGC**T**CATACTGA	5464
2,4-DB resistance 3-ketoacyl-CoA thiolase B *Mangifera indica* Tyr42Term TAT-TAG	TCACAATTACGAGTCCGCTCTTGCCGCATCAGTATGTGCTGCAGGGGATAGCGCCGCATA**G**CATAGGGCTTCTGTTTATGGAGACGATGTGGTGATTGTGGCAGCTCATCGTACTGCACTT	5465
	AAGTGCAGTACGATGAGCTGCCACAATCACCACATCGTCTCCATAAACAGAAGCCCTATG**C**TATGCGGCGCTATCCCCTGCAGCACATACTGATGCGGCAAGAGCGGACTCGTAATTGTGA	5466
	GCCGCATA**G**CATAGGGC	5467
	GCCCTATG**C**TATGCGGC	5468
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Tyr22Term TAC-TAG	GAAGGCGATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTTCCGCTTA**G**ACAAATGAATCTTCGCTCTCTGCATCGGTTTGTGCAGCTGGGGATAGTGCTTCGTATCAA	5469
	TTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAGCGAAGATTCATTTGT**C**TAAGCGGAAGAAGAAGGCCGGAGATGATGTAGCAAAATGCTCTGCCTGTTGATCGCCTTC	5470
	TCCGCTTA**G**ACAAATGA	5471
	TCATTTGT**C**TAAGCGGA	5472
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTTCCGCTTACACAAAT**T**AATCTTCGCTCTCTGCATCGGTTTGTGCAGCTGGGGATAGTGCTTCGTATCAAAGGACAT	5473
	ATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAGCGAAGATT**A**ATTTGTGTAAGCGGAAGAAGAAGGCCGGAGATGATGTAGCAAAATGCTCTGCCTGTTGAT	5474
	ACACAAAT**T**AATCTTCG	5475
	CGAAGATT**A**ATTTGTGT	5476

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Ser27Term TCG-TAG	GGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATCTT**A**GCTCTCTGCATCGGTTTGTGCAGCTGGGGATAGTGCTTCGTATCAAAGGACATCGGTGTT	5477
	AACACCGATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAGC**T**AAGATTCATTTGTGTAAGCGGAAGAAGAAGGCCGGAGATGATGTAGCAAAATGCTCTGCC	5478
	TGAATCTT**A**GCTCTCTG	5479
	CAGAGAGC**T**AAGATTCA	5480
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATCTTCGCTCTCTGCAT**A**GGTTTGTGCAGCTGGGGATAGTGCTTCGTATCAAAGGACATCGGTGTTTGGAGATGATGT	5481
	ACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAAACC**T**ATGCAGAGAGCGAAGATTCATTTGTGTAAGCGGAAGAAGAAGGCCGGAGATGATGTAGCA	5482
	CTCTGCAT**A**GGTTTGTG	5483
	CACAAACC**T**ATGCAGAG	5484
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Cys33Term TGT-TGA	TCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATCTTCGCTCTCTGCATCGGTTTG**A**GCAGCTGGGGATAGTGCTTCGTATCAAAGGACATCGGTGTTTGGAGATGATGTCGTGATT	5485
	AATCACGACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCACTATCCCCAGCTGC**T**CAAACCGATGCAGAGAGCGAAGATTCATTTGTGTAAGCGGAAGAAGAAGGCCGGAGATGA	5486
	TCGGTTTG**A**GCAGCTGG	5487
	CCAGCTGC**T**CAAACCGA	5488
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Tyr22Term TAT-TAG	GAAGGCAATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTTCGGCTTA**G**AGCCATGAATCTTCGCTCTCTGCATCGGTTTGTGCAGCTGGGGATAGTGCGTCGTATCAA	5489
	TTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAGCGAAGATTCATGGCT**C**TAAGCCGAAGATGAAGGCCGGAGATGATGTAGCAGAATGCTCTGCCTGTTGATTGCCTTC	5490
	TCGGCTTA**G**AGCCATGA	5491
	TCATGGCT**C**TAAGCCGA	5492

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATTAATCTTCGCTCTCTGCATCGGTTTGTGCAGCTGGGGATAGTGCGTCGTATCAAAGAACGT	5493
	ACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAGCGAAGATTAATGGCTATAAGCCGAAGATGAAGGCCGGAGATGATGTAGCAGAATGCTCTGCCTGTTGAT	5494
	ATAGCCATTAATCTTCG	5495
	CGAAGATTAATGGCTAT	5496
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Ser27Term TCG-TAG	GGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTAGCTCTCTGCATCGGTTTGTGCAGCTGGGGATAGTGCGTCGTATCAAAGAACGTCGGTGTT	5497
	AACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAGCTAAGATTCATGGCTATAAGCCGAAGATGAAGGCCGGAGATGATGTAGCAGAATGCTCTGCC	5498
	TGAATCTTAGCTCTCTG	5499
	CAGAGAGCTAAGATTCA	5500
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTCGCTCTCTGCATAGGTTTGTGCAGCTGGGGATAGTGCGTCGTATCAAAGAACGTCGGTGTTTGGAGATGATGT	5501
	ACATCATCTCCAAACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCTATGCAGAGAGCGAAGATTCATGGCTATAAGCCGAAGATGAAGGCCGGAGATGATGTAGCA	5502
	CTCTGCATAGGTTTGTG	5503
	CACAAACCTATGCAGAG	5504
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Cys33Term TGT-TGA	TCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTCGCTCTCTGCATCGGTTTGAGCAGCTGGGGATAGTGCGTCGTATCAAAGAACGTCGGTGTTTGGAGATGATGTCGTGATA	5505
	TATCACGACATCATCTCCAAACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCATGGCTATAAGCCGAAGATGAAGGCCGGAGATGA	5506
	TCGGTTTGAGCAGCTGG	5507
	CCAGCTGCTCAAACCGA	5508
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln5Term CAG-TAG	TCATAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTATGGCAACTCATTAGCAAACGCAACCTCCTTCCGATTTTCCCGCTCTTGCCGATGAAAATTCCCAGATTCCAG	5509
	CTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGGAAGGAGGTTGCGTTTGCTAATGAGTTGCCATAGCAGCTCACTAACCTTGGAAGAATCCAAGCGGCAAAAGAGACTATGA	5510

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAACTCATTAGCAAACG	5511
	CGTTTGCTAATGAGTTG	5512
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln6Term CAA-TAA	TAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTATGGCAACTCATCAGTAAACGCAACCTCCTTCCGATTTTCCCGCTCTTGCCGATGAAAATTCCCAGATTCCAGGTT	5513
	AACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGGAAGGAGGTTGCGTTTACTGATGAGTTGCCATAGCAGCTCACTAACCTTGGAAGAATCCAAGCGGCAAAAGAGACTA	5514
	CTCATCAGTAAACGCAA	5515
	TTGCGTTTACTGATGAG	5516
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln8Term CAA-TAA	CTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTATGGCAACTCATCAGCAAACGTAACCTCCTTCCGATTTTCCCGCTCTTGCCGATGAAAATTCCCAGATTCCAGGTTCAATTT	5517
	AAATTGAACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGGAAGGAGGTTACGTTTGCTGATGAGTTGCCATAGCAGCTCACTAACCTTGGAAGAATCCAAGCGGCAAAAG	5518
	AGCAAACGTAACCTCCT	5519
	AGGAGGTTACGTTTGCT	5520
2,4 DB resistance Pex14 *Arabidopsis thaliana* Glu19Term GAA-TAA	GCTGCTATGGCAACTCATCAGCAAACGCAACCTCCTTCCGATTTTCCCGCTCTTGCCGATTAAAATTCCCAGATTCCAGGTTCAATTTACACCTTCTAATCATTATTTCTTAATTTTTCTT	5521
	AAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAATTGAACCTGGAATCTGGGAATTTTAATCGGCAAGAGCGGGAAAATCGGAAGGAGGTTGCGTTTGCTGATGAGTTGCCATAGCAGC	5522
	TTGCCGATTAAAATTCC	5523
	GGAATTTTAATCGGCAA	5524
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln22Term CAG-TAG	GCAACTCATCAGCAAACGCAACCTCCTTCCGATTTTCCCGCTCTTGCCGATGAAAATTCCTAGATTCCAGGTTCAATTTACACCTTCTAATCATTATTTCTTAATTTTTCTTTGGTGGATT	5525
	AATCCACCAAAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAATTGAACCTGGAATCTAGGAATTTTCATCGGCAAGAGCGGGAAAATCGGAAGGAGGTTGCGTTTGCTGATGAGTTGC	5526
	AAAATTCCTAGATTCCA	5527
	TGGAATCTAGGAATTTT	5528

Example 8

Production of albino mutants for the analysis of photosynthetic processes

Plant productivity is limited by resources available and the ability of plants to harness these resources. The conversion of light to chemical energy, which is then used to synthesize carbohydrates, fatty acids, sugars, amino acids and other compounds, requires a complex system which combines the light harvesting apparatus of pigments and proteins. The value of light energy to the plant can only be realized when it is efficiently converted into chemical energy by photosynthesis and fed into various biochemical processes. Significant effort has therefore been directed at studying photosynthetic processes in plants in order to improve productivity and/or the efficiency of photosynthesis. The analysis of the photosynthetic process is substantially aided by the ability to produce albino plants.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 18
Oligonucleotides to produce albino plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
White leaves Immutans *Arabidopsis thaliana* Ser5Term TCA-TGA	TTCTTTCCTGTGAAATTATCTGCTCAAATCTTTGGTTCCTGACGGAG ATGGCGGCGATTT**G**AGGCATCTCCTCTGGTACGTTGACGATTTCA CGGCCTTTGGTTACTCTTCGACGCTCTAG	5529
	CTAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTA CCAGAGGAGATGCCT**C**AAATCGCCGCCATCTCCGTCAGGAACCAA AGATTTGAGCAGATAATTTCACAGGAAAGAA	5530
	GGCGATTT**G**AGGCATCT	5531
	AGATGCCT**C**AAATCGCC	5532
White leaves Immutans *Arabidopsis thaliana* Leu12Term TTG-TAG	GCTCAAATCTTTGGTTCCTGACGGAGATGGCGGCGATTTCAGGCA TCTCCTCTGGTACGT**A**GACGATTTCACGGCCTTTGGTTACTCTTCG ACGCTCTAGAGCCGCCGTTTCGTACAGCTC	5533
	GAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAGAGTAACCAAA GGCCGTGAAATCGTC**T**ACGTACCAGAGGAGATGCCTGAAATCGCC GCCATCTCCGTCAGGAACCAAAGATTTGAGC	5534
	TGGTACGT**A**GACGATTT	5535
	AAATCGTC**T**ACGTACCA	5536
White leaves Immutans *Arabidopsis thaliana* Ser15Term TCA-TGA	TTTGGTTCCTGACGGAGATGGCGGCGATTTCAGGCATCTCCTCTG GTACGTTGACGATTT**G**ACGGCCTTTGGTTACTCTTCGACGCTCTAG AGCCGCCGTTTCGTACAGCTCCTCTCACCG	5537
	CGGTGAGAGGAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAG AGTAACCAAAGGCCGT**C**AAATCGTCAACGTACCAGAGGAGATGCC TGAAATCGCCGCCATCTCCGTCAGGAACCAAA	5538
	GACGATTT**G**ACGGCCTT	5539
	AAGGCCGT**C**AAATCGTC	5540
White leaves Immutans *Arabidopsis thaliana* Arg22Term CGA-TGA	GCGGCGATTTCAGGCATCTCCTCTGGTACGTTGACGATTTCACGG CCTTTGGTTACTCTT**T**GACGCTCTAGAGCCGCCGTTTCGTACAGCT CCTCTCACCGATTGCTTCATCATCTTCCTC	5541
	GAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTGTACGAAACG GCGGCTCTAGAGCGTC**A**AAGAGTAACCAAAGGCCGTGAAATCGTC AACGTACCAGAGGAGATGCCTGAAATCGCCGC	5542
	TTACTCTT**T**GACGCTCT	5543
	AGAGCGTC**A**AAGAGTAA	5544

White leaves Immutans *Arabidopsis thaliana* Arg25Term AGA-TGA	TCAGGCATCTCCTCTGGTACGTTGACGATTTCACGGCCTTTGGTTACTCTTCGACGCTCTTGAGCCGCCGTTTCGTACAGCTCCTCTCACCGATTGCTTCATCATCTTCCTCTCTCTTCTC	5545
	GAGAAGAGAGAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTGTACGAAACGGCGGCTCAAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTACCAGAGGAGATGCCTGA	5546
	GACGCTCTTGAGCCGCC	5547
	GGCGGCTCAAGAGCGTC	5548
White leaves Immutans *Lycopersicon esculentum* Gly11Term GGA-TGA	GATTCTTGTGGGAAGGAAGAAGGATCAAGAATGGCGATTTCGATTTCTGCTATGAGTTTTTGAACCTCAGTTTCTTCATATTCTTGTTTTAGAGCTAGGAGTTTTGAGAAGTCATCAGTTT	5549
	AAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGAATATGAAGAAACTGAGGTTCAAAAACTCATAGCAGAAATCGAAATCGCCATTCTTGATCCTTCTTCCTTCCCACAAGAATC	5550
	TGAGTTTTTGAACCTCA	5551
	TGAGGTTCAAAAACTCA	5552
White leaves Immutans *Lycopersicon esculentum* Ser13Term TCA-TGA	GTGGGAAGGAAGAAGGATCAAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGGAACCTGAGTTTCTTCATATTCTTGTTTTAGAGCTAGGAGTTTTGAGAAGTCATCAGTTTTATGCAA	5553
	TTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGAATATGAAGAAACTCAGGTTCCAAAACTCATAGCAGAAATCGAAATCGCCATTCTTGATCCTTCTTCCTTCCCAC	5554
	TGGAACCTGAGTTTCTT	5555
	AAGAAACTCAGGTTCCA	5556
White leaves Immutans *Lycopersicon esculentum* Ser16Term TCA-TGA	AAGAAGGATCAAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGGAACCTCAGTTTCTTGATATTCTTGTTTTAGAGCTAGGAGTTTTGAGAAGTCATCAGTTTTATGCAATTCCCAGAA	5557
	TTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGAATATCAAGAAACTGAGGTTCCAAAACTCATAGCAGAAATCGAAATCGCCATTCTTGATCCTTCTT	5558
	AGTTTCTTGATATTCTT	5559
	AAGAATATCAAGAAACT	5560
White leaves Immutans *Lycopersicon esculentum* Tyr17Term TAT-TAG	AGGATCAAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGGAACCTCAGTTTCTTCATAGTCTTGTTTTAGAGCTAGGAGTTTTGAGAAGTCATCAGTTTTATGCAATTCCCAGAACCCA	5561
	TGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGACTATGAAGAAACTGAGGTTCCAAAACTCATAGCAGAAATCGAAATCGCCATTCTTGATCCT	5562
	TCTTCATAGTCTTGTTT	5563
	AAACAAGACTATGAAGA	5564

White leaves Immutans *Lycopersicon esculentum* Cys19Term TGT-TGA	AAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGGAACCTCAGTTTCTTCATATTCTTG**A**TTTAGAGCTAGGAGTTTTGAGAAGTCATCAGTTTTATGCAATTCCCAGAACCCATGTCGG	5565
	CCGACATGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAA**T**CAAGAATATGAAGAAACTGAGGTTCCAAAACTCATAGCAGAAATCGAAATCGCCATTCTT	5566
	TATTCTTG**A**TTTAGAGC	5567
	GCTCTAAA**T**CAAGAATA	5568
White leaves Immutans *Capsicum annuum* Ser13Term TCA-TGA	CGCGTCCGATAAAAAAATCAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAACTT**G**AGTTTCTTCTTCATATTCAGCATTTTTGTGCAATTCCAAGAACCCATTTTGTTTGAATTC	5569
	GAATTCAAACAAAATGGGTTCTTGGAATTGCACAAAAATGCTGAATATGAAGAAGAAACT**C**AAGTTCGAAAACTCATAGCAGATATGGAAATCGCCATTCTTGATTTTTTTATCGGACGCG	5570
	TCGAACTT**G**AGTTTCTT	5571
	AAGAAACT**C**AAGTTCGA	5572
White leaves Immutans *Capsicum annuum* Ser17Term TCA-TGA	AAAAATCAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTT**G**ATATTCAGCATTTTTGTGCAATTCCAAGAACCCATTTTGTTTGAATTCTCTATTTTCACT	5573
	AGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAATTGCACAAAAATGCTGAATAT**C**AAGAAGAAACTGAAGTTCGAAAACTCATAGCAGATATGGAAATCGCCATTCTTGATTTTT	5574
	TTCTTCTT**G**ATATTCAG	5575
	CTGAATAT**C**AAGAAGAA	5576
White leaves Immutans *Capsicum annuum* Ser19Term TCA-TGA	CAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCATATT**G**AGCATTTTTGTGCAATTCCAAGAACCCATTTTGTTTGAATTCTCTATTTTCACTTAGGAA	5577
	TTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAATTGCACAAAAATGCT**C**AATATGAAGAAGAAACTGAAGTTCGAAAACTCATAGCAGATATGGAAATCGCCATTCTTG	5578
	TTCATATT**G**AGCATTTT	5579
	AAAATGCT**C**AATATGAA	5580
White leaves Immutans *Capsicum annuum* Leu21Term TTG-TAG	CGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCATATTCAGCATTTT**A**GTGCAATTCCAAGAACCCATTTTGTTTGAATTCTCTATTTTCACTTAGGAATTCTCATAG	5581
	CTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAATTGCAC**T**AAAATGCTGAATATGAAGAAGAAACTGAAGTTCGAAAACTCATAGCAGATATGGAAATCG	5582
	AGCATTTT**A**GTGCAATT	5583
	AATTGCAC**T**AAAATGCT	5584

White leaves Immutans *Capsicum annuum* Cys22Term TGC-TGA	TTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCATATTCAGCATTTTTGTG**A**AATTCCAAGAACCCATTTTGTTTGAATTCTCTATTTTCACTTAGGAATTCTCATAGAACT	5585
	AGTTCTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAATT**T**CACAAAAATGCTGAATATGAAGAAGAAACTGAAGTTCGAAAACTCATAGCAGATATGGAA	5586
	TTTTTGTG**A**AATTCCAA	5587
	TTGGAATT**T**CACAAAAA	5588
White leaves Immutans *Oryza sativa* Glu22Term GAG-TAG	TTCGGCACGAGGGAGAAGGAGCAGACCGAGGTGGCCGTCGAGGAGTCCTTCCCCTTCAGG**T**AGACGGCTCCTCCTGACGAGCCACTGGTCACCGCCGAGGAGAGCTGGGTGGTTAAGCTCG	5589
	CGAGCTTAACCACCCAGCTCTCCTCGGCGGTGACCAGTGGCTCGTCAGGAGGAGCCGTCT**A**CCTGAAGGGGAAGGACTCCTCGACGGCCACCTCGGTCTGCTCCTTCTCCCTCGTGCCGAA	5590
	CCTTCAGG**T**AGACGGCT	5591
	AGCCGTCT**A**CCTGAAGG	5592
White leaves Immutans *Oryza sativa* Glu28Term CAG-TAG	GAGCAGACCGAGGTGGCCGTCGAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGAC**T**AGCCACTGGTCACCGCCGAGGAGAGCTGGGTGGTTAAGCTCGAGCAGTCCGTGAACATTT	5593
	AAATGTTCACGGACTGCTCGAGCTTAACCACCCAGCTCTCCTCGGCGGTGACCAGTGGCT**A**GTCAGGAGGAGCCGTCTCCCTGAAGGGGAAGGACTCCTCGACGGCCACCTCGGTCTGCTC	5594
	CTCCTGAC**T**AGCCACTG	5595
	CAGTGGCT**A**GTCAGGAG	5596
White leaves Immutans *Oryza sativa* Glu34Term GAG-TAG	GTCGAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCACCGCC**T**AGGAGAGCTGGGTGGTTAAGCTCGAGCAGTCCGTGAACATTTTCCTCACGGAGTCAGTCA	5597
	TGACTGACTCCGTGAGGAAAATGTTCACGGACTGCTCGAGCTTAACCACCCAGCTCTCCT**A**GGCGGTGACCAGTGGCTCGTCAGGAGGAGCCGTCTCCCTGAAGGGGAAGGACTCCTCGAC	5598
	TCACCGCC**T**AGGAGAGC	5599
	GCTCTCCT**A**GGCGGTGA	5600
White leaves Immutans *Oryza sativa* Glu35Term GAG-TAG	GAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCACCGCCGAG**T**AGAGCTGGGTGGTTAAGCTCGAGCAGTCCGTGAACATTTTCCTCACGGAGTCAGTCATCA	5601
	TGATGACTGACTCCGTGAGGAAAATGTTCACGGACTGCTCGAGCTTAACCACCCAGCTCT**A**CTCGGCGGTGACCAGTGGCTCGTCAGGAGGAGCCGTCTCCCTGAAGGGGAAGGACTCCTC	5602
	CCGCCGAG**T**AGAGCTGG	5603
	CCAGCTCT**A**CTCGGCGG	5604

White leaves Immutans *Oryza sativa* Trp37Term TGG-TGA	CTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCACCGCCGAGGAGAGCTGAGTGGTTAAGCTCGAGCAGTCCGTGAACATTTTCCTCACGGAGTCAGTCATCACGATACTT	5605
	AAGTATCGTGATGACTGACTCCGTGAGGAAAATGTTCACGGACTGCTCGAGCTTAACCACTCAGCTCTCCTCGGCGGTGACCAGTGGCTCGTCAGGAGGAGCCGTCTCCCTGAAGGGGAAG	5606
	GAGAGCTGAGTGGTTAA	5607
	TTAACCACTCAGCTCTC	5608
White leaves Immutans *Triticum aestivum* Trp22Term TGG-TGA	TCCGGAGGAGGAAGGGGGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTGAGTCGTCAGATTCGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATACTC	5609
	GAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTGCTCGAATCTGACGACTCAGTCGCCGTCCTCGCCGGCGAGGGTGAGCTCCTCGTCGAATCCCCCTTCCTCCTCCGGA	5610
	GGCGACTGAGTCGTCAG	5611
	CTGACGACTCAGTCGCC	5612
White leaves Immutans *Triticum aestivum* Arg25Term AGA-TGA	GAGGAAGGGGGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTGGGTCGTCTGATTCGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATACTCGATATTC	5613
	GAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTGCTCGAATCAGACGACCCAGTCGCCGTCCTCGCCGGCGAGGGTGAGCTCCTCGTCGAATCCCCCTTCCTC	5614
	GGGTCGTCTGATTCGAG	5615
	CTCGAATCAGACGACCC	5616
White leaves Immutans *Triticum aestivum* Glu27Term GAG-TAG	GGGGGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTGGGTCGTCAGATTCTAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATACTCGATATTCTGTATC	5617
	GATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTGCTAGAATCTGACGACCCAGTCGCCGTCCTCGCCGGCGAGGGTGAGCTCCTCGTCGAATCCCCC	5618
	TCAGATTCTAGCAGTCC	5619
	GGACTGCTAGAATCTGA	5620
White leaves Immutans *Triticum aestivum* Gln28Term CAG-TAG	GGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTGGGTCGTCAGATTCGAGTAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATACTCGATATTCTGTATCGTG	5621
	CACGATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTACTCGAATCTGACGACCCAGTCGCCGTCCTCGCCGGCGAGGGTGAGCTCCTCGTCGAATCC	5622
	GATTCGAGTAGTCCTTC	5623
	GAAGGACTACTCGAATC	5624

White leaves Immutans *Triticum aestivum* Tyr46Term TAT-TAG	CGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATACTCGATATTCTGTAGCGTGACCGCGACTACGCAAGGTTCTTCGTGCTCGAGACCATCGCCAGGGTGCCCTATTTC	5625
	GAAATAGGGCACCCTGGCGATGGTCTCGAGCACGAAGAACCTTGCGTAGTCGCGGTCACGCTACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTGCTCG	5626
	ATTCTGTAGCGTGACCG	5627
	CGGTCACGCTACAGAAT	5628

Example 9

Altering amino acid content of plants

Another aim of biotechnology is to generate plants, especially crop plants, with added value traits. An example of such a trait is improved nutritional quality in food crops. For example, lysine, tryptophan and threonine, which are essential amino acids in the diet of humans and many animals, are limiting nutrients in most cereal crops. Consequently, grain-based diets, such as those based on corn, barley, wheat, rice, maize, millet, sorghum, and the like, must be supplemented with more expensive synthetic amino acids or amino-acid-containing oilseed protein meals. Increasing the lysine content of these grains or of any of the feed component crops would result in significant added value.

Naturally occurring mutants of plants that have different levels of particular essential amino acids have been identified. However, these mutants are generally not the result of increased free amino acid, but are instead the result of shifts in the overall protein profile of the grain. For example, in maize, reduced levels of lysine-deficient endosperm proteins (prolamines) are complemented by elevated levels of more lysine-rich proteins (albumins, globulins and glutelins). While nutritionally superior, these mutants are associated with reduced yields and poor grain quality, limiting their agronomic usefulness.

An alternative approach is to generate plants with mutations that render key amino acid biosynthetic enzymes insensitive to feedback inhibition. Many such mutations are known and mutation results in increased free amino acid. The increased production can optionally be coupled to increased expression of an abundant storage protein comprising the chosen amino acid. Alternatively, a normally abundant protein can be engineered to contain more of the target amino acid.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that remove feedback inhibition in plant amino acid biosynthetic enzymes.

Table 19
Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS *Arabidopsis thaliana* Arg77His CGT-CAT	TATCCTCCAGGATCTTAAGATTTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCATAGAAACTGTAGCAACATCGGTGTTGCACAGATCGTGGCGGCTAAGTGGTCCAACAACCC	5629
	GGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACCGATGTTGCTACAGTTTCTATGGGCTTTAATGCTCAGCTGACGGACGAAATTAGGAGGAAATCTTAAGATCCTGGAGGATA	5630
	TAAAGCCCATAGAAACT	5631
	AGTTTCTATGGGCTTTA	5632
Met Overproduction CGS *Arabidopsis thaliana* Ser81Asn AGC-AAC	TCTTAAGATTTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCGTAGAAACTGTAACAACATCGGTGTTGCACAGATCGTGGCGGCTAAGTGGTCCAACAACCCATCCTCCGCGTT	5633
	AACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACCGATGTTGTTACAGTTTCTACGGGCTTTAATGCTCAGCTGACGGACGAAATTAGGAGGAAATCTTAAGA	5634
	AAACTGTAACAACATCG	5635
	CGATGTTGTTACAGTTT	5636
Met Overproduction CGS *Arabidopsis thaliana* Gly84Ser GGT-AGT	TTTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCGTAGAAACTGTAGCAACATCAGTGTTGCACAGATCGTGGCGGCTAAGTGGTCCAACAACCCATCCTCCGCGTTACCTTCGG	5637
	CCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACTGATGTTGCTACAGTTTCTACGGGCTTTAATGCTCAGCTGACGGACGAAATTAGGAGGAAA	5638
	GCAACATCAGTGTTGCA	5639
	TGCAACACTGATGTTGC	5640
Met Overproduction CGS *Arabidopsis thaliana* Gly84Asp GGT-GAT	TTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCGTAGAAACTGTAGCAACATCGATGTTGCACAGATCGTGGCGGCTAAGTGGTCCAACAACCCATCCTCCGCGTTACCTTCGGC	5641
	GCCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACATCGATGTTGCTACAGTTTCTACGGGCTTTAATGCTCAGCTGACGGACGAAATTAGGAGGAA	5642
	CAACATCGATGTTGCAC	5643
	GTGCAACATCGATGTTG	5644

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS *Fragraria vesca* Arg73His CGC-CAC	TATCGTCACTCATCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCACCGCAACTGCAGCAACATCGGCGTCGCGCAGATCGTCGCGGCTTCGTGGTCCAACAAAGA	5645
	TCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGCCGATGTTGCTGCAGTTGCGGTGGGCCTTGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAAGCGGAGGATGAGTGACGATA	5646
	CAAGGCCCACCGCAACT	5647
	AGTTGCGGTGGGCCTTG	5648
Met Overproduction CGS *Fragraria vesca* Ser77Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCGCAACTGCAACAACATCGGCGTCGCGCAGATCGTCGCGGCTTCGTGGTCCAACAAAGACTCCGACCTTTC	5649
	GAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGCCGATGTTGTTGCAGTTGCGGCGGGCCTTGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAAGCGGAGGA	5650
	CAACTGCAACAACATCG	5651
	CGATGTTGTTGCAGTTG	5652
Met Overproduction CGS *Fragraria vesca* Gly80Ser GGC-AGC	TTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCGCAACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCGGCTTCGTGGTCCAACAAAGACTCCGACCTTTCGGCGGTGC	5653
	GCACCGCCGAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGGGCCTTGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAA	5654
	GCAACATCAGCGTCGCG	5655
	CGCGACGCTGATGTTGC	5656
Met Overproduction CGS *Fragraria vesca* Gly80Asp GGC-GAC	TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCGCAACTGCAGCAACATCGACGTCGCGCAGATCGTCGCGGCTTCGTGGTCCAACAAAGACTCCGACCTTTCGGCGGTGCC	5657
	GGCACCGCCGAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGTCGATGTTGCTGCAGTTGCGGCGGGCCTTGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGA	5658
	CAACATCGACGTCGCGC	5659
	GCGCGACGTCGATGTTG	5660
Met Overproduction CGS *Glycine max* Arg68His CGC-CAC	TCTCCTCCCTCATCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGAGCCGCAACTGCAGCAACATCGGCGTCGCGCAAATCGTCGCCGCTTCGTGGTCGAACAACAG	5661
	CTGTTGTTCGACCACGAAGCGGCGACGATTTGCGCGACGCCGATGTTGCTGCAGTTGCGGCTCGCCTTGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAAGCGGAGGATGAGGGAGGAGA	5662
	CCAAGGCGAGCCGCAAC	5663

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTGCGGCTCGCCTTGG	5664
Met Overproduction CGS *Glycine max* Ser72Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCGCAACTGCAACAACATCGGCGTCGCGCAAATCGTCGCCGCTTCGTGGTCGAACAACAGCGACAACTCTCC	5665
	GGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGCGACGATTTGCGCGACGCCGATGTTGTTGCAGTTGCGGCGCGCCTTGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAAGCGGAGGA	5666
	CAACTGCAACAACATCG	5667
	CGATGTTGTTGCAGTTG	5668
Met Overproduction CGS *Glycine max* Gly75Ser GGC-AGC	TTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCGCAACTGCAGCAACATCAGCGTCGCGCAAATCGTCGCCGCTTCGTGGTCGAACAACAGCGACAACTCTCCGGCCGCCG	5669
	CGGCGGCCGGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGCGACGATTTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGCGCCTTGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA	5670
	GCAACATCAGCGTCGCG	5671
	CGCGACGCTGATGTTGC	5672
Met Overproduction CGS *Glycine max* Gly75Asp GGC-GAC	TCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCGCAACTGCAGCAACATCGACGTCGCGCAAATCGTCGCCGCTTCGTGGTCGAACAACAGCGACAACTCTCCGGCCGCCGG	5673
	CCGGCGGCCGGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGCGACGATTTGCGCGACGTCGATGTTGCTGCAGTTGCGGCGCGCCTTGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGA	5674
	CAACATCGACGTCGCGC	5675
	GCGCGACGTCGATGTTG	5676
Met Overproduction CGS *Solanum tuberosum* Arg70His AGG-CAC	TGTCTTCTCTGATTTTCAGGTTTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGCTCACAGGAATTGCAGCAATATTGGCGTGGCTCAAGTTGTGGCGGCTTCCTGGTCTAACAACCA	5677
	TGGTTGTTAGACCAGGAAGCCGCCACAACTTGAGCCACGCCAATATTGCTGCAATTCCTGTGAGCCTTAATGCTTAGCTGCCTCACGAAATTAGGAGGAAACCTGAAAATCAGAGAAGACA	5678
	TAAGGCTCACAGGAATT	5679
	AATTCCTGTGAGCCTTA	5680
Met Overproduction CGS *Solanum tuberosum* Ser74Asn AGC-AAC	TTTTCAGGTTTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGCTAGGAGGAATTGCAACAATATTGGCGTGGCTCAAGTTGTGGCGGCTTCCTGGTCTAACAACCAAGCCGGTCCTGA	5681
	TCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCCACAACTTGAGCCACGCCAATATTGTTGCAATTCCTCCTAGCCTTAATGCTTAGCTGCCTCACGAAATTAGGAGGAAACCTGAAAA	5682

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAATTGCAACAATATTG	5683
	CAATATTGTTGCAATTC	5684
Met Overproduction CGS *Solanum tuberosum* Gly77Ser GGC-AGC	TTTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGCTAGGAGG AATTGCAGCAATATTAGCGTGGCTCAAGTTGTGGCGGCTTCCTGG TCTAACAACCAAGCCGGTCCTGAATTCACTC	5685
	GAGTGAATTCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCC ACAACTTGAGCCACGCTAATATTGCTGCAATTCCTCCTAGCCTTAA TGCTTAGCTGCCTCACGAAATTAGGAGGAAA	5686
	GCAATATTAGCGTGGCT	5687
	AGCCACGCTAATATTGC	5688
Met Overproduction CGS *Solanum tuberosum* Gly77Asp GGC-GAC	TTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGCTAGGAGGA ATTGCAGCAATATTGACGTGGCTCAAGTTGTGGCGGCTTCCTGGT CTAACAACCAAGCCGGTCCTGAATTCACTCC	5689
	GGAGTGAATTCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGC CACAACTTGAGCCACGTCAATATTGCTGCAATTCCTCCTAGCCTTA ATGCTTAGCTGCCTCACGAAATTAGGAGGAA	5690
	CAATATTGACGTGGCTC	5691
	GAGCCACGTCAATATTG	5692
Met Overproduction CGS *Mesembryanthemum crystallinum* Arg73His CGC-CAC	CTTCCTCTCTTATCCTTCGCTTTCCTCCCAACTTTGTCCGTCAGCT CAGCACCAAGGCTCGCCACAACTGCAGCAACATTGGTGTCGCAC AGGTCGTCGCTGCCTCCTGGTCCAACAACTC	5693
	GAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACACCAAT GTTGCTGCAGTTGTGGCGAGCCTTGGTGCTGAGCTGACGGACAA AGTTGGGAGGAAAGCGAAGGATAAGAGAGGAAG	5694
	GGCTCGCCACAACTGCA	5695
	TGCAGTTGTGGCGAGCC	5696
Met Overproduction CGS *Mesembryanthemum crystallinum* Ser77Asn AGC-AAC	TCCTTCGCTTTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGG CTCGCCGCAACTGCAACAACATTGGTGTCGCACAGGTCGTCGCT GCCTCCTGGTCCAACAACTCCGATGCCGGCGC	5697
	GCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCT GTGCGACACCAATGTTGTTGCAGTTGCGGCGAGCCTTGGTGCTG AGCTGACGGACAAAGTTGGGAGGAAAGCGAAGGA	5698
	CAACTGCAACAACATTG	5699
	CAATGTTGTTGCAGTTG	5700

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS *Mesembryanthemum crystallinum* Gly80Ser GGT-AGT	TTTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGCAACTGCAGCAACATTAGTGTCGCACAGGTCGTCGCTGCCTCCTGGTCCAACAACTCCGATGCCGGCGCCACCTCTT	5701
	AAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACACTAATGTTGCTGCAGTTGCGGCGAGCCTTGGTGCTGAGCTGACGGACAAAGTTGGGAGGAAA	5702
	GCAACATTAGTGTCGCA	5703
	TGCGACACTAATGTTGC	5704
Met Overproduction CGS *Mesembryanthemum crystallinum* Gly80Asp GGT-GAT	TTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGCAACTGCAGCAACATTGATGTCGCACAGGTCGTCGCTGCCTCCTGGTCCAACAACTCCGATGCCGGCGCCACCTCTTG	5705
	CAAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACATCAATGTTGCTGCAGTTGCGGCGAGCCTTGGTGCTGAGCTGACGGACAAAGTTGGGAGGAA	5706
	CAACATTGATGTCGCAC	5707
	GTGCGACATCAATGTTG	5708
Met Overproduction CGS *Zea mays* Arg41His CGC-CAC	CCTCTGCTACCATCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACACCGCAACTGCAGCAACATCGGCGTCGCGCAGATCGTCGCCGCCGCGTGGTCCGACTGCCC	5709
	GGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGCCGATGTTGCTGCAGTTGCGGTGTGCCTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAAGCGGAGGATGGTAGCAGAGG	5710
	CAAGGCACACCGCAACT	5711
	AGTTGCGGTGTGCCTTG	5712
Met Overproduction CGS *Zea mays* Ser45Asn AGC-AAC	TCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGCAACTGCAACAACATCGGCGTCGCGCAGATCGTCGCCGCCGCGTGGTCCGACTGCCCCGCCGCTCGCCC	5713
	GGGCGAGCGGCGGGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGCCGATGTTGTTGCAGTTGCGGCGTGCCTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAAGCGGAGGA	5714
	CAACTGCAACAACATCG	5715
	CGATGTTGTTGCAGTTG	5716
Met Overproduction CGS *Zea mays* Gly48Ser GGC-AGC	TTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGCAACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCCGCCGCGTGGTCCGACTGCCCCGCCGCTCGCCCCCACTTAG	5717
	CTAAGTGGGGGCGAGCGGCGGGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGTGCCTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAA	5718
	GCAACATCAGCGTCGCG	5719

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCGACGCTGATGTTGC	5720
Met Overproduction CGS *Zea mays* Gly48Asp GGC-GAC	TTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGCAACTGCAGCAACATCGACGTCGCGCAGATCGTCGCCGCCGCGTGGTCCGACTGCCCCGCCGCTCGCCCCCACTTAGG	5721
	CCTAAGTGGGGGCGAGCGGCGGGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGTCGATGTTGCTGCAGTTGCGGCGTGCCTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAA	5722
	CAACATCGACGTCGCGC	5723
	GCGCGACGTCGATGTTG	5724
Met Overproduction TS *Arabidopsis thaliana* Leu205Arg CTT-CGT	GTATGAATGATCTGTGGGTGAAACACTGTGGGATTAGTCATACAGGAAGTTTCAAGGATCGTGGAATGACTGTTTTGGTTAGTCAAGTTAATCGTCTGAGAAAGATGAAACGACCTGTGGT	5725
	ACCACAGGTCGTTTCATCTTTCTCAGACGATTAACTTGACTAACCAAAACAGTCATTCCACGATCCTTGAAACTTCCTGTATGACTAATCCCACAGTGTTTCACCCACAGATCATTCATAC	5726
	CAAGGATCGTGGAATGA	5727
	TCATTCCACGATCCTTG	5728
Met Overproduction TS *Solanum tuberosum* Leu198Arg CTT-CGT	GCATGACTGATTTGTGGGTCAAACACTGTGGGATTAGCCATACTGGTAGTTTTAAGGATCGTGGGATGACTGTTTTGGTGAGTCAAGTTAATCGCTTGCGGAAAATGCATAAACCGGTTGT	5729
	ACAACCGGTTTATGCATTTTCCGCAAGCGATTAACTTGACTCACCAAAACAGTCATCCCACGATCCTTAAAACTACCAGTATGGCTAATCCCACAGTGTTTGACCCACAAATCAGTCATGC	5730
	TAAGGATCGTGGGATGA	5731
	TCATCCCACGATCCTTA	5732
Lys Overproduction DHPS *Zea mays* Ser157Asn AGC-AAC	TCATTGGGCACACAGTGAACTGCTTTGGCTCTAGAATCAAAGTGATAGGCAACACAGGAAACAACTCAACCAGAGAAGCCGTCCACGCAACAGAACAGGGATTTGCTGTTGGCATGCATGC	5733
	GCATGCATGCCAACAGCAAATCCCTGTTCTGTTGCGTGGACGGCTTCTCTGGTTGAGTTGTTTCCTGTGTTGCCTATCACTTTGATTCTAGAGCCAAAGCAGTTCACTGTGTGCCCAATGA	5734
	CACAGGAAACAACTCAA	5735
	TTGAGTTGTTTCCTGTG	5736
Lys Overproduction DHPS *Zea mays* Ala166Val GCA-GAA	GCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACCAGAGAAGCCGTCCACGAAACAGAACAGGGATTTGCTGTTGGCATGCATGCGGCTCTCCACATCAATCCTTACTACGG	5737
	CCGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGCAAATCCCTGTTCTGTTTCGTGGACGGCTTCTCTGGTTGAGTTGCTTCCTGTGTTGCCTATCACTTTGATTCTAGAGC	5738

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGTCCACGAAACAGAAC	5739
	GTTCTGTTTCGTGGACG	5740
Lys Overproduction DHPS *Zea mays* Ala166Thr GCA-ACA	GGCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACC AGAGAAGCCGTCCACACAACAGAACAGGGATTTGCTGTTGGCAT GCATGCGGCTCTCCACATCAATCCTTACTACG	5741
	CGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGCAA ATCCCTGTTCTGTTGTGTGGACGGCTTCTCTGGTTGAGTTGCTTC CTGTGTTGCCTATCACTTTGATTCTAGAGCC	5742
	CCGTCCACACAACAGAA	5743
	TTCTGTTGTGTGGACGG	5744
Lys Overproduction DHPS *Oryza sativa* Ser124Asn AGT-AAT	TTATTGGGCATACAGTTAACTGCTTTGGCACTAAAATTAAAGTGGT CGGCAACACAGGAAATAACTCAACAAGGGAGGCTATTCACGCAAC TGAGCAGGGATTCGCTGTAGGTATGCACGC	5745
	GCGTGCATACCTACAGCGAATCCCTGCTCAGTTGCGTGAATAGCC TCCCTTGTTGAGTTATTTCCTGTGTTGCCGACCACTTTAATTTTAGT GCCAAAGCAGTTAACTGTATGCCCAATAA	5746
	CACAGGAAATAACTCAA	5747
	TTGAGTTATTTCCTGTG	5748
Lys Overproduction DHPS *Oryza sativa* Ala133Val GCA-GTA	GCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACAA GGGAGGCTATTCACGTAACTGAGCAGGGATTCGCTGTAGGTATG CACGCGGCTCTCCACATCAATCCTTACTACGG	5749
	CCGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGC GAATCCCTGCTCAGTTACGTGAATAGCCTCCCTTGTTGAGTTACTT CCTGTGTTGCCGACCACTTTAATTTTAGTGC	5750
	TATTCACGTAACTGAGC	5751
	GCTCAGTTACGTGAATA	5752
Lys Overproduction DHPS *Oryza sativa* Ala133Thr GCA-ACA	GGCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACA AGGGAGGCTATTCACACAACTGAGCAGGGATTCGCTGTAGGTAT GCACGCGGCTCTCCACATCAATCCTTACTACG	5753
	CGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGCG AATCCCTGCTCAGTTGTGTGAATAGCCTCCCTTGTTGAGTTACTTC CTGTGTTGCCGACCACTTTAATTTTAGTGCC	5754
	CTATTCACACAACTGAG	5755
	CTCAGTTGTGTGAATAG	5756
Lys Overproduction DHPS 1 *Triticum aestivum* Ser165Asn AGT-AAT	TCATCGGGCATACTGTTAACTGCTTTGGAGCCAACATTAAAGTGAT AGGCAACACGGGAAATAACTCAACCAGAGAAGCTGTTCACGCGA CAGAGCAGGGATTTGCTGTTGGCATGCATGC	5757

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCATGCATGCCAACAGCAAATCCCTGCTCTGTCGCGTGAACAGCTTCTCTGGTTGAGTTATTTCCCGTGTTGCCTATCACTTTAATGTTGGCTCCAAAGCAGTTAACAGTATGCCCGATGA	5758
	CACGGGAAATAACTCAA	5759
	TTGAGTTATTTCCCGTG	5760
Lys Overproduction DHPS 1 *Triticum aestivum* Ala174Val GCG-GTG	GAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACCAGAGAAGCTGTTCACGTGACAGAGCAGGGATTTGCTGTTGGCATGCATGCAGCTCTTCATGTCAATCCTTACTACGG	5761
	CCGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAAATCCCTGCTCTGTCACGTGAACAGCTTCTCTGGTTGAGTTACTTCCCGTGTTGCCTATCACTTTAATGTTGGCTC	5762
	TGTTCACGTGACAGAGC	5763
	GCTCTGTCACGTGAACA	5764
Lys Overproduction DHPS 1 *Triticum aestivum* Ala174Thr GCG-ACG	GGAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACCAGAGAAGCTGTTCACACGACAGAGCAGGGATTTGCTGTTGGCATGCATGCAGCTCTTCATGTCAATCCTTACTACG	5765
	CGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAAATCCCTGCTCTGTCGTGTGAACAGCTTCTCTGGTTGAGTTACTTCCCGTGTTGCCTATCACTTTAATGTTGGCTCC	5766
	CTGTTCACACGACAGAG	5767
	CTCTGTCGTGTGAACAG	5768
Lys Overproduction DHPS 2 *Triticum aestivum* Ser154Asn AGT-AAT	TCATCGGGCACACTGTTAACTGCTTTGGAACTAACATTAAAGTGATAGGCAACACGGGAAATAACTCAACTAGAGAAGCGATTCACGCTTCAGAGCAGGGATTTGCTGTTGGCATGCATGC	5769
	GCATGCATGCCAACAGCAAATCCCTGCTCTGAAGCGTGAATCGCTTCTCTAGTTGAGTTATTTCCCGTGTTGCCTATCACTTTAATGTTAGTTCCAAAGCAGTTAACAGTGTGCCCGATGA	5770
	CACGGGAAATAACTCAA	5771
	TTGAGTTATTTCCCGTG	5772
Lys Overproduction DHPS 2 *Triticum aestivum* Ala163Val GCT-GTT	GAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACTAGAGAAGCGATTCACGTTTCAGAGCAGGGATTTGCTGTTGGCATGCATGCAGCTCTCCATGTCAATCCTTACTATGG	5773
	CCATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAAATCCCTGCTCTGAAACGTGAATCGCTTCTCTAGTTGAGTTACTTCCCGTGTTGCCTATCACTTTAATGTTAGTTC	5774
	GATTCACGTTTCAGAGC	5775
	GCTCTGAAACGTGAATC	5776

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lys Overproduction DHPS 2 *Triticum aestivum* Ala163Thr GCT-ACT	GGAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACTAGAGAAGCGATTCAC**A**CTTCAGAGCAGGGATTTGCTGTTGGCATGCATGCAGCTCTCCATGTCAATCCTTACTATG	5777
	CATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAAATCCCTGCTCTGAAG**T**GTGAATCGCTTCTCTAGTTGAGTTACTTCCCGTGTTGCCTATCACTTTAATGTTAGTTCC	5778
	CGATTCAC**A**CTTCAGAG	5779
	CTCTGAAG**T**GTGAATCG	5780
Lys Overproduction DHPS *Coix lacryma-jobi* Ser154Asn AGT-AAT	CTCATTGGGCATACTGTGAACTGCTTTGGCTCTAGAATTAAAGTGATAGGCAACACAGGAA**A**TAACTCAACCAGAGAAGCTGTTCACGCAACAGAGCAGGGATTTGCTGTTGGCATGCATG	5781
	CATGCATGCCAACAGCAAATCCCTGCTCTGTTGCGTGAACAGCTTCTCTGGTTGAGTTA**T**TTCCTGTGTTGCCTATCACTTTAATTCTAGAGCCAAAGCAGTTCACAGTATGCCCAATGAG	5782
	CACAGGAA**A**TAACTCAA	5783
	TTGAGTTA**T**TTCCTGTG	5784
Lys Overproduction DHPS *Coix lacryma-jobi* Ala163Val GCA-GTA	GCTCTAGAATTAAAGTGATAGGCAACACAGGAAGTAACTCAACCAGAGAAGCTGTTCACG**T**AACAGAGCAGGGATTTGCTGTTGGCATGCATGCAGCTCTCCACATCAATCCTTACTATGG	5785
	CCATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAAATCCCTGCTCTGTT**A**CGTGAACAGCTTCTCTGGTTGAGTTACTTCCTGTGTTGCCTATCACTTTAATTCTAGAGC	5786
	TGTTCACG**T**AACAGAGC	5787
	GCTCTGTT**A**CGTGAACA	5788
Lys Overproduction DHPS *Coix lacryma-jobi* Ala163Thr GCA-ACA	GGCTCTAGAATTAAAGTGATAGGCAACACAGGAAGTAACTCAACCAGAGAAGCTGTTCAC**A**CAACAGAGCAGGGATTTGCTGTTGGCATGCATGCAGCTCTCCACATCAATCCTTACTATG	5789
	CATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAAATCCCTGCTCTGTTG**T**GTGAACAGCTTCTCTGGTTGAGTTACTTCCTGTGTTGCCTATCACTTTAATTCTAGAGCC	5790
	CTGTTCAC**A**CAACAGAG	5791
	CTCTGTTG**T**GTGAACAG	5792
Lys Overproduction DHPS *Nicotiana tabacum* Ser136Asn AGC-AAC	TCATTGGTCACACAGTCAATTGTTTTGGAGGGTCCATCAAAGTCATCGGGAACACTGGAA**A**CAACTCCACAAGGGAAGCAATCCATGCAACTGAACAGGGATTTGCTGTAGGTATGCATGC	5793
	GCATGCATACCTACAGCAAATCCCTGTTCAGTTGCATGGATTGCTTCCCTTGTGGAGTTG**T**TTCCAGTGTTCCCGATGACTTTGATGGACCCTCCAAAACAATTGACTGTGTGACCAATGA	5794
	CACTGGAA**A**CAACTCCA	5795

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGGAGTTGTTTCCAGTG	5796
Lys Overproduction DHPS *Nicotiana tabacum* Ala145Val GCA-GTA	GAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCACAA GGGAAGCAATCCATGTAACTGAACAGGGATTTGCTGTAGGTATGC ATGCAGCTCTTCACATTAATCCCTACTATGG	5797
	CCATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCA AATCCCTGTTCAGTTACATGGATTGCTTCCCTTGTGGAGTTGCTTC CAGTGTTCCCGATGACTTTGATGGACCCTC	5798
	AATCCATGTAACTGAAC	5799
	GTTCAGTTACATGGATT	5800
Lys Overproduction DHPS *Nicotiana tabacum* Ala145Thr GCA-ACA	GGAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCAC AAGGGAAGCAATCCATACAACTGAACAGGGATTTGCTGTAGGTAT GCATGCAGCTCTTCACATTAATCCCTACTATG	5801
	CATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCAA ATCCCTGTTCAGTTGTATGGATTGCTTCCCTTGTGGAGTTGCTTCC AGTGTTCCCGATGACTTTGATGGACCCTCC	5802
	CAATCCATACAACTGAA	5803
	TTCAGTTGTATGGATTG	5804
Lys Overproduction DHPS *Arabidopsis thaliana* Ser142Asn AGC-AAC	TTATAGGCCATACCGTTAACTGTTTTGGCGGAAGCATCAAAGTCAT TGGAAACACTGGAAACAATTCGACTAGAGAAGCAATCCACGCGAC TGAACAAGGATTCGCGGTTGGAATGCATGC	5805
	GCATGCATTCCAACCGCGAATCCTTGTTCAGTCGCGTGGATTGCT TCTCTAGTCGAATTGTTTCCAGTGTTTCCAATGACTTTGATGCTTC CGCCAAAACAGTTAACGGTATGGCCTATAA	5806
	CACTGGAAACAATTCGA	5807
	TCGAATTGTTTCCAGTG	5808
Lys Overproduction DHPS *Arabidopsis thaliana* Ala151Val GCG-GTG	GCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACTA GAGAAGCAATCCACGTGACTGAACAAGGATTCGCGGTTGGAATGC ATGCTGCTCTTCATATAAACCCTTACTATGG	5809
	CCATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCG AATCCTTGTTCAGTCACGTGGATTGCTTCTCTAGTCGAATTGCTTC CAGTGTTTCCAATGACTTTGATGCTTCCGC	5810
	AATCCACGTGACTGAAC	5811
	GTTCAGTCACGTGGATT	5812
Lys Overproduction DHPS *Arabidopsis thaliana* Ala151Thr GCG-ACG	GGCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACT AGAGAAGCAATCCACACGACTGAACAAGGATTCGCGGTTGGAATG CATGCTGCTCTTCATATAAACCCTTACTATG	5813
	CATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCGA ATCCTTGTTCAGTCGTGTGGATTGCTTCTCTAGTCGAATTGCTTCC AGTGTTTCCAATGACTTTGATGCTTCCGCC	5814

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAATCCACACGACTGAA	5815
	TTCAGTCGTGTGGATTG	5816
Lys Overproduction DHPS *Glycine max* Ser103Asn AGC-AAC	TTATTGCTCATACAGTCAACTGTTTTGGTGGGAAAATTAAGGTTATT GGAAATACTGGAAACAACTCCACCAGGGAAGCAATTCATGCCACT GAGCAGGGTTTTGCTGTTGGAATGCATGC	5817
	GCATGCATTCCAACAGCAAAACCCTGCTCAGTGGCATGAATTGCT TCCCTGGTGGAGTTGTTTCCAGTATTTCCAATAACCTTAATTTTCC CACCAAAACAGTTGACTGTATGAGCAATAA	5818
	TACTGGAAACAACTCCA	5819
	TGGAGTTGTTTCCAGTA	5820
Lys Overproduction DHPS *Glycine max* Ala112Val GCC-GTC	GTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACCA GGGAAGCAATTCATGTCACTGAGCAGGGTTTTGCTGTTGGAATGC ATGCTGCCCTTCACATAAACCCTTACTATGG	5821
	CCATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCA AAACCCTGCTCAGTGACATGAATTGCTTCCCTGGTGGAGTTGCTT CCAGTATTTCCAATAACCTTAATTTTCCCAC	5822
	AATTCATGTCACTGAGC	5823
	GCTCAGTGACATGAATT	5824
Lys Overproduction DHPS *Glycine max* Ala112Thr GCC-ACC	GGTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACC AGGGAAGCAATTCATACCACTGAGCAGGGTTTTGCTGTTGGAATG CATGCTGCCCTTCACATAAACCCTTACTATG	5825
	CATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCAA AACCCTGCTCAGTGGTATGAATTGCTTCCCTGGTGGAGTTGCTTC CAGTATTTCCAATAACCTTAATTTTCCCACC	5826
	CAATTCATACCACTGAG	5827
	CTCAGTGGTATGAATTG	5828
Trp Overproduction AS *Arabidopsis thaliana* Asp341Asn GAC-AAC	CTTGCAGGAGACATATTTCAGATCGTGCTGAGTCAACGTTTTGAG CGGCGAACATTTGCAAACCCCTTTGAAGTTTATAGAGCACTAAGA GTTGTGAATCCAAGTCCGTATATGGGTTATT	5829
	AATAACCCATATACGGACTTGGATTCACAACTCTTAGTGCTCTATA AACTTCAAAGGGGTTTGCAAATGTTCGCCGCTCAAAACGTTGACT CAGCACGATCTGAAATATGTCTCCTGCAAG	5830
	CATTTGCAAACCCCTTT	5831
	AAAGGGGTTTGCAAATG	5832
Trp Overproduction AS *Nicotiana tabacum* Asp326Asn GAC-AAC	GCTGCAGGAGACATATTTCAAATCGTTTTAAGTCAACGCTTTGAGA GAAGAACATTTGCTAACCCATTTGAAGTGTACAGAGCATTAAGAAT TGTGAATCCAAGCCCATATATGACTTACA	5833

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTAAGTCATATATGGGCTTGGATTCACAATTCTTAATGCTCTGTACACTTCAAATGGGTTAGCAAATGTTCTTCTCTCAAAGCGTTGACTTAAAACGATTTGAAATATGTCTCCTGCAGC	5834
	CATTTGCTAACCCATTT	5835
	AAATGGGTTAGCAAATG	5836
Trp Overproduction AS *Oryza sativa* Asp323Asn GAC-AAC	CTAGCTGGTGACATTTTTCAAGTAGTCTTAAGCCAGCGTTTTGAGAGGCGTACATTTGCTAACCCCTTTGAGGTGTACCGTGCATTGCGTATTGTCAATCCTAGTCCTTATATGGCCTATC	5837
	GATAGGCCATATAAGGACTAGGATTGACAATACGCAATGCACGGTACACCTCAAAGGGGTTAGCAAATGTACGCCTCTCAAAACGCTGGCTTAAGACTACTTGAAAAATGTCACCAGCTAG	5838
	CATTTGCTAACCCCTTT	5839
	AAAGGGGTTAGCAAATG	5840
Trp Overproduction AS *Ruta graveolens* Asp354Asn GAC-AAC	CTTGCTGGTGACATATTCCAGATCGTACTAAGTCAGCGTTTTGAAAGGCGAACGTTCGCAAACCCATTTGAAATCTATAGATCACTGAGGATTGTTAATCCAAGCCCATATATGACTTATT	5841
	AATAAGTCATATATGGGCTTGGATTAACAATCCTCAGTGATCTATAGATTTCAAATGGGTTTGCGAACGTTCGCCTTTCAAAACGCTGACTTAGTACGATCTGGAATATGTCACCAGCAAG	5842
	CGTTCGCAAACCCATTT	5843
	AAATGGGTTTGCGAACG	5844
Trp Overproduction AS *Catharanthus roseus* Asp354Asn GAT-AAT	CTGGCTGGGGACATATTCCAGCTTGTCCTAAGTCAGCGTTTTGAACGGCGAACATTTGCAAATCCATTTGAAGTCTACCGAGCATTGAGAATTGTCAACCCAAGTCCATATATGACTTATT	5845
	AATAAGTCATATATGGACTTGGGTTGACAATTCTCAATGCTCGGTAGACTTCAAATGGATTTGCAAATGTTCGCCGTTCAAAACGCTGACTTAGGACAAGCTGGAATATGTCCCCAGCCAG	5846
	CATTTGCAAATCCATTT	5847
	AAATGGATTTGCAAATG	5848

Example 10

Production of modified starch in plants

A principal aim of biotechnology is the improvement of crop plants for food value, agriculture, and to produce a range of plant-derived raw materials. Along with oils, fats and proteins, polysaccharides constitute the main raw materials derived from plants, and apart from cellulose, the storage polymer starch is the most important polysaccharide raw material. Starch is derived from a range of plants, but maize is the most important cultivated plant for the production of starch.

The polysaccharide starch is a polymer made up of glucose molecules. However, starch is not a homogeneous raw material and is, in fact, a highly complex mixture of various types of molecules which differ from each other, for example, in their degree of polymerization and in the degree of branching of the glucose chains. For example, amylose-starch is a basically non-branched polymer made up of α-1,4-glycosidically branched glucose molecules, and amylopectin-starch is a complex mixture of variously branched glucose chains. The branching results from additional α-1,6-glycosidic linkages. In plants from which starch is typically isolated, for example maize or potato, the starch is approximately 25% amylose-starch and 75% amylopectin-starch.

In maize, various mutants in starch metabolism are known, for example *waxy*, *sugary*, *shrunken* and *opaque-2*. In addition to producing a modified starch, these mutations greatly improve grain quality in maize, and thus expand the use of maize not only as the food but also for the important industrial materials in food chemistry. It would therefore be advantageous to be able readily to obtain mutants in these genes in particular maize genotypes as well as other plants. Such plants can be obtained, for example, using traditional breeding methods and through specific genetic modification by means of recombinant DNA techniques.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 20
Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Arabidopsis thaliana* Ala99Lys GCA-AAA	GAACTTGAGACTGAGAAAAGGGATCCAAGGACAGTTGCTTCCATT ATTCTTGGAGGTGGAAAAGGAACTCGACTCTTTCCTCTCACAAAA CGCCGCGCCAAGCCTGCCGTTCCTATCGGGG	5849
	CCCCGATAGGAACGGCAGGCTTGGCGCGGCGTTTTGTGAGAGGA AAGAGTCGAGTTCCTTTTCCACCTCCAAGAATAATGGAAGCAACT GTCCTTGGATCCCTTTTCTCAGTCTCAAGTTC	5850
	GAGGTGGAAAAGGAACT	5851
	AGTTCCTTTTCCACCTC	5852
Increased Starch ADPGPP *Arabidopsis thaliana* Pro127Leu CCA-CTA	CAAAACGCCGCGCCAAGCCTGCCGTTCCTATCGGGGGAGCCTAT AGGTTGATAGATGTACTAATGAGCAATTGTATTAACAGCGGAATCA ACAAAGTCTACATACTCACACAATATAACTC	5853
	GAGTTATATTGTGTGAGTATGTAGACTTTGTTGATTCCGCTGTTAA TACAATTGCTCATTAGTACATCTATCAACCTATAGGCTCCCCCGAT AGGAACGGCAGGCTTGGCGCGGCGTTTTG	5854
	AGATGTACTAATGAGCA	5855
	TGCTCATTAGTACATCT	5856
Increased Starch ADPGPP *Arabidopsis thaliana* Gly162Asn GGA-AAT	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC TTACAACTCCAATAATCTTGGCTTTGGAGATGGCTATGTTGAGGTT CTTGCGGCCACTCAAACGCCAGGAGAATC	5857
	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAAAGCCAAGATTATTGGAGTTGTAAGCACGGGCTAAATGC CTGTTCAATGATGCTGAGTTATATTGTGTGA	5858
	CTCCAATAATCTTGGCT	5859
	AGCCAAGATTATTGGAG	5860
Increased Starch ADPGPP *Arabidopsis thaliana* Gly162Asn GGA-AAC	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC TTACAACTCCAATAACCTTGGCTTTGGAGATGGCTATGTTGAGGTT CTTGCGGCCACTCAAACGCCAGGAGAATC	5861
	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAAAGCCAAGGTTATTGGAGTTGTAAGCACGGGCTAAATGC CTGTTCAATGATGCTGAGTTATATTGTGTGA	5862
	CTCCAATAACCTTGGCT	5863
	AGCCAAGGTTATTGGAG	5864

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Arabidopsis thaliana* Asn100Lys AAT-AAA	GTTTGAGAGAAGAAAGGTAGACCCGCAAAATGTGGCTGCAATCAT TCTAGGAGGAGGCAA**A**GGAGCTAAACTCTTCCCTCTTACAATGAG AGCCGCAACACCAGCTGTAAATATTCATCTT	5865
	AAGATGAATATTTACAGCTGGTGTTGCGGCTCTCATTGTAAGAGG GAAGAGTTTAGCTCC**T**TTGCCTCCTCCTAGAATGATTGCAGCCAC ATTTTGCGGGTCTACCTTTCTTCTCTCAAAC	5866
	GGAGGCAA**A**GGAGCTAA	5867
	TTAGCTCC**T**TTGCCTCC	5868
Increased Starch ADPGPP *Arabidopsis thaliana* Pro128Leu CCG-CTG	CTTGTGTCTTCAAATTATGTTAGGTTCCTGTTGGTGGATGCTACAG GCTGATCGATATCC**T**GATGAGTAACTGTATTAACAGCTGCATCAAC AAGATATTTGTGCTGACACAGTTCAACTC	5869
	GAGTTGAACTGTGTCAGCACAAATATCTTGTTGATGCAGCTGTTAA TACAGTTACTCATC**A**GGATATCGATCAGCCTGTAGCATCCACCAA CAGGAACCTAACATAATTTGAAGACACAAG	5870
	CGATATCC**T**GATGAGTA	5871
	TACTCATC**A**GGATATCG	5872
Increased Starch ADPGPP *Arabidopsis thaliana* Gly163Asn GGC-AAT	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC TTATTTTGGGAAT**AAT**ATAAACTTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	5873
	GCTGAGAGTTATTATTGTCATAGTGTTTGTACCTCTACGAAACCAC CTCCAAAGTTTAT**ATT**ATTCCCAAAATAAGTTCGTGCTAAATGTCG ATTAAGGGAAGCTGAGTTGAACTGTGTCA	5874
	TGGGAAT**AAT**ATAAACT	5875
	AGTTTAT**ATT**ATTCCCA	5876
Increased Starch ADPGPP *Arabidopsis thaliana* Gly163Asn GGC-AAC	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC TTATTTTGGGAAT**AAC**ATAAACTTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	5877
	GCTGAGAGTTATTATTGTCATAGTGTTTGTACCTCTACGAAACCAC CTCCAAAGTTTAT**GTT**ATTCCCAAAATAAGTTCGTGCTAAATGTCG ATTAAGGGAAGCTGAGTTGAACTGTGTCA	5878
	TGGGAAT**AAC**ATAAACT	5879
	AGTTTAT**GTT**ATTCCCA	5880
Increased Starch ADPGPP *Lycopersicon esculentum* Val94Lys GTT-AAA	TTGAGGAACAACCAACGGCAGATCCAAAAGCTGTTGCCTCTGTCA TTCTAGGTGGTGGT**AAA**GGAACTCGTCTTTTTCCTCTTACAAGCA GAAGAGCTAAACCAGCTGTTCCTATTGGTGG	5881
	CCACCAATAGGAACAGCTGGTTTAGCTCTTCTGCTTGTAAGAGGA AAAAGACGAGTTCC**TTT**ACCACCACCTAGAATGACAGAGGCAACA GCTTTTGGATCTGCCGTTGGTTGTTCCTCAA	5882
	TGGTGGT**AAA**GGAACTC	5883

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAGTTCC**TTT**ACCACCA	5884
Increased Starch ADPGPP *Lycopersicon esculentum* Pro122Leu CCA-CAA	CAAGCAGAAGAGCTAAACCAGCTGTTCCTATTGGTGGTTGTTACCGGCTAATTGATGTAC**A**AATGAGTAACTGCATTAACAGTGGCATACGGAAAATTTTCATCTTAACACAGTTCAATTC	5885
	GAATTGAACTGTGTTAAGATGAAAATTTTCCGTATGCCACTGTTAATGCAGTTACTCATT**T**GTACATCAATTAGCCGGTAACAACCACCAATAGGAACAGCTGGTTTAGCTCTTCTGCTTG	5886
	TGATGTAC**A**AATGAGTA	5887
	TACTCATT**T**GTACATCA	5888
Increased Starch ADPGPP *Lycopersicon esculentum* Gly158Asn GGA-AAT	CACAGTTCAATTCCTTTTCCCTCAATCGTCACCTTGCCCGCACGTATAATTTTGGAAAT**AAT**GTGGGTTTTGGAGATGGATTTGTGGAGGTTTTAGCTGCAACCCAGACTCCAGGGGATGC	5889
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCATCTCCAAAACCCAC**ATT**ATTTCCAAAATTATACGTGCGGGCAAGGTGACGATTGAGGGAAAAGGAATTGAACTGTG	5890
	TGGAAAT**AAT**GTGGGTT	5891
	AACCCAC**ATT**ATTTCCA	5892
Increased Starch ADPGPP *Lycopersicon esculentum* Gly158Asn GGA-AAC	CACAGTTCAATTCCTTTTCCCTCAATCGTCACCTTGCCCGCACGTATAATTTTGGAAAT**AAC**GTGGGTTTTGGAGATGGATTTGTGGAGGTTTTAGCTGCAACCCAGACTCCAGGGGATGC	5893
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCATCTCCAAAACCCAC**GTT**ATTTCCAAAATTATACGTGCGGGCAAGGTGACGATTGAGGGAAAAGGAATTGAACTGTG	5894
	TGGAAAT**AAC**GTGGGTT	5895
	AACCCAC**GTT**ATTTCCA	5896
Increased Starch ADPGPP *Cicer arietinum* Ala101Lys GCT-AAA	ACGTAGATTTGGAAAAAAGAGACCCAAGTACAGTTGTAGCAATTATACTAGGTGGAGGT**AAA**GGAACTCGTCTCTTCCCTCTCACCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGG	5897
	CCTCCAATTGGAACAGCAGGCTTGGCTCGTCGCTTGGTGAGAGGGAAGAGACGAGTTCC**TTT**ACCTCCACCTAGTATAATTGCTACAACTGTACTTGGGTCTCTTTTTTCCAAATCTACGT	5898
	TGGAGGT**AAA**GGAACTC	5899
	GAGTTCC**TTT**ACCTCCA	5900

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Cicer arietinum* Pro129Leu CCA-CTA	CCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGGTGCTTATAGGCTGATAGATGTAC**T**AATGAGTAACTGCATCAATAGTGGGATCAACAAAGTATACATTCTCACTCAATTTAATTC	5901
	GAATTAAATTGAGTGAGAATGTATACTTTGTTGATCCCACTATTGATGCAGTTACTCATT**A**GTACATCTATCAGCCTATAAGCACCTCCAATTGGAACAGCAGGCTTGGCTCGTCGCTTGG	5902
	AGATGTAC**T**AATGAGTA	5903
	TACTCATT**A**GTACATCT	5904
Increased Starch ADPGPP *Cicer arietinum* Gly165Asn GGA-AAT	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTATAACTCTGGTACT**AAT**GTCACTTTTGGAGATGGCTATGTTGAGGTTCTTGCAGCAACTCAAACTCCAGGGGAGCA	5905
	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCATCTCCAAAAGTGAC**ATT**AGTACCAGAGTTATAAGCACGTGCAATATGCCTGTTGAGTGAGGCTGAATTAAATTGAG	5906
	TGGTACT**AAT**GTCACTT	5907
	AAGTGAC**ATT**AGTACCA	5908
Increased Starch ADPGPP *Cicer arietinum* Gly165Asn GGA-AAC	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTATAACTCTGGTACT**AAC**GTCACTTTTGGAGATGGCTATGTTGAGGTTCTTGCAGCAACTCAAACTCCAGGGGAGCA	5909
	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCATCTCCAAAAGTGAC**GTT**AGTACCAGAGTTATAAGCACGTGCAATATGCCTGTTGAGTGAGGCTGAATTAAATTGAG	5910
	TGGTACT**AAC**GTCACTT	5911
	AAGTGAC**GTT**AGTACCA	5912
Increased Starch ADPGPP *Ipomoea batatas* Ala94Lys GCA-AAA	ATATTGGAGAGGCGTCGGGCAAACCCTAAGAATGTGGCTGCAATCATACTGCCAGGCGGT**AA**AGGGACACACCTATTCCCTCTCACCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAG	5913
	CTCCAAGTGGAACAGCAGGGGTTGCAGCTCGATTGGTGAGAGGGAATAGGTGTGTCCCT**TT**ACCGCCTGGCAGTATGATTGCAGCCACATTCTTAGGGTTTGCCCGACGCCTCTCCAATAT	5914
	CAGGCGGT**AA**AGGGACA	5915
	TGTCCCT**TT**ACCGCCTG	5916
Increased Starch ADPGPP *Ipomoea batatas* Pro122Leu CCA-CTA	CCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAGGATGCTATAGGTTGATCGACATTC**T**AATGAGCAACTGCATCAACAGCGGGGTTAACAAGATCTTTGTGCTGACCCAGTTCAATTC	5917
	GAATTGAACTGGGTCAGCACAAAGATCTTGTTAACCCCGCTGTTGATGCAGTTGCTCATT**A**GAATGTCGATCAACCTATAGCATCCTCCAAGTGGAACAGCAGGGGTTGCAGCTCGATTGG	5918
	CGACATTC**T**AATGAGCA	5919

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCTCATT**A**GAATGTCG	5920
Increased Starch ADPGPP *Ipomoea batatas* Gly157Asn GGT-AAT	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTACCGTCTTTGGCAAT**AAT**GTGAGCTTCGGAGATGGATTTGTTGAGGTGCTGGCTGCAACCCAAACACAAGGGGAAAC	5921
	GTTTCCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCATCTCCGAAGCTCAC**ATT**ATTGCCAAAGACGGTACGGGAAATGTGACGGTTAAGAGAAGCTGAATTGAACTGGGTCA	5922
	TGGCAAT**AAT**GTGAGCT	5923
	AGCTCAC**ATT**ATTGCCA	5924
Increased Starch ADPGPP *Ipomoea batatas* Gly157Asn GGT-AAC	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTACCGTCTTTGGCAAT**AAC**GTGAGCTTCGGAGATGGATTTGTTGAGGTGCTGGCTGCAACCCAAACACAAGGGGAAAC	5925
	GTTTCCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCATCTCCGAAGCTCAC**GTT**ATTGCCAAAGACGGTACGGGAAATGTGACGGTTAAGAGAAGCTGAATTGAACTGGGTCA	5926
	TGGCAAT**AAC**GTGAGCT	5927
	AGCTCAC**GTT**ATTGCCA	5928
Increased Starch ADPGPP *Oryza sativa* Thr96Lys ACC-AAA	CATTCCGGAGGAACTTTGCGGATCCAAATGAGGTTGCTGCTGTTATATTGGGTGGTGGCA**AA**GGGACTCAACTTTTTCCTCTCACAAGCACAAGGGCCACGCCTGCTGTTCCTATTGGAGG	5929
	CCTCCAATAGGAACAGCAGGCGTGGCCCTTGTGCTTGTGAGAGGAAAAAGTTGAGTCCC**TT**TGCCACCACCCAATATAACAGCAGCAACCTCATTTGGATCCGCAAAGTTCCTCCGGAATG	5930
	TGGTGGCA**AA**GGGACTC	5931
	GAGTCCC**TT**TGCCACCA	5932
Increased Starch ADPGPP *Oryza sativa* Pro124Leu CCC-CTC	CAAGCACAAGGGCCACGCCTGCTGTTCCTATTGGAGGATGCTATAGGCTTATCGATATCC**T**CATGAGCAACTGTTTCAACAGTGGCATAAACAAGATATTCATAATGACTCAATTCAACTC	5933
	GAGTTGAATTGAGTCATTATGAATATCTTGTTTATGCCACTGTTGAAACAGTTGCTCATG**A**GGATATCGATAAGCCTATAGCATCCTCCAATAGGAACAGCAGGCGTGGCCCTTGTGCTTG	5934
	CGATATCC**T**CATGAGCA	5935
	TGCTCATG**A**GGATATCG	5936
Increased Starch ADPGPP *Oryza sativa* Gly159Asn GGA-AAT	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTACGTACCTTGGTGGT**AAT**ATCAACTTTACTGATGGTTCTGTTGAGGTATTAGCCGCTACACAAATGCCTGGGGAGGC	5937
	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCATCAGTAAAGTTGAT**ATT**ACCACCAAGGTACGTACGATGAATGTGACGATTAAGAGATGCTGAGTTGAATTGAGTCA	5938

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGGTGGT**AAT**ATCAACT	5939
	AGTTGAT**ATT**ACCACCA	5940
Increased Starch ADPGPP *Oryza sativa* Gly159Asn GGA-AAC	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGGTGGT**AAC**ATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC	5941
	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGAT**GTT**ACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA	5942
	TGGTGGT**AAC**ATCAACT	5943
	AGTTGAT**GTT**ACCACCA	5944
Increased Starch ADPGPP *Triticum aestivum* Thr80Lys ACC-AAA	GTCCTTCAGGAGGATTAAGCGATCCGAACGAGGTTGCGGCCGTC ATACTCGGCGGCGGCA**AA**GGGACTCAGCTCTTCCCACTCACGAG CACAAGGGCCACACCTGCTGTTCCTATTGGAGG	5945
	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTCGTGAGTGG GAAGAGCTGAGTCCC**TT**TGCCGCCGCCGAGTATGACGGCCGCAA CCTCGTTCGGATCGCTTAATCCTCCTGAAGGAC	5946
	CGGCGGCA**AA**GGGACTC	5947
	GAGTCCC**TT**TGCCGCCG	5948
Increased Starch ADPGPP *Triticum aestivum* Pro108Leu CCC-CTC	CGAGCACAAGGGCCACACCTGCTGTTCCTATTGGAGGATGTTACA GGCTCATCGACATTC**T**CATGAGCAACTGCTTCAACAGTGGCATCA ACAAGATATTCGTCATGACCCAGTTCAACTC	5949
	GAGTTGAACTGGGTCATGACGAATATCTTGTTGATGCCACTGTTG AAGCAGTTGCTCATG**A**GAATGTCGATGAGCCTGTAACATCCTCCA ATAGGAACAGCAGGTGTGGCCCTTGTGCTCG	5950
	CGACATTC**T**CATGAGCA	5951
	TGCTCATG**A**GAATGTCG	5952
Increased Starch ADPGPP *Triticum aestivum* Gly143Asn GGA-AAT	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG**AAT**ATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5953
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGAT**ATT**CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	5954
	CGGCGGG**AAT**ATCAATT	5955
	AATTGAT**ATT**CCCGCCG	5956
Increased Starch ADPGPP *Triticum aestivum* Gly143Asn GGA-AAC	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG**AAC**ATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5957

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGAT**GTT**CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	5958
	CGGCGGG**AAC**ATCAATT	5959
	AATTGAT**GTT**CCCGCCG	5960
Increased Starch ADPGPP *Oryza sativa* Thr95Lys ACT-AAA	CCTCCCGAAAGAATTATGCTGATGCAAGCCACGTTTCTGCTGTCA TTTTGGGTGGAGGCA**AA**GGAGTTCAACTCTTTCCTCTGACAAGCA CAAGGGCTACCCCCGCTGTTCCTGTTGGAGG	5961
	CCTCCAACAGGAACAGCGGGGGTAGCCCTTGTGCTTGTCAGAGG AAAGAGTTGAACTCC**TT**TGCCTCCACCCAAAATGACAGCAGAAAC GTGGCTTGCATCAGCATAATTCTTTCGGGAGG	5962
	TGGAGGCA**AA**GGAGTTC	5963
	GAACTCC**TT**TGCCTCCA	5964
Increased Starch ADPGPP *Oryza sativa* Pro123Leu CCT-CTT	CAAGCACAAGGGCTACCCCCGCTGTTCCTGTTGGAGGATGTTACA GGCTTATTGACATCC**T**TATGAGCAATTGCTTCAATAGCGGAATAAA TAAAATATTTGTGATGACTCAGTTCAATTC	5965
	GAATTGAACTGAGTCATCACAAATATTTTATTTATTCCGCTATTGAA GCAATTGCTCATA**A**GGATGTCAATAAGCCTGTAACATCCTCCAACA GGAACAGCGGGGGTAGCCCTTGTGCTTG	5966
	TGACATCC**T**TATGAGCA	5967
	TGCTCATA**A**GGATGTCA	5968
Increased Starch ADPGPP *Oryza sativa* Gly158Asn GGG-AAT	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATAC ATACCTTGGTGGG**AAT**ATCAACTTTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCTGACGAACC	5969
	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGAT**ATT**CCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGAACTGAGTCA	5970
	TGGTGGG**AAT**ATCAACT	5971
	AGTTGAT**ATT**CCCACCA	5972
Increased Starch ADPGPP *Oryza sativa* Gly158Asn GGG-AAC	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATAC ATACCTTGGTGGG**AAC**ATCAACTTTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCTGACGAACC	5973
	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGAT**GTT**CCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGAACTGAGTCA	5974
	TGGTGGG**AAC**ATCAACT	5975
	AGTTGAT**GTT**CCCACCA	5976

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Triticum aestivum* Thr99Lys ACC-AAA	CCTTCCGCAGGAATTACGCCGATCCGAACGAGGTCGCGGCCGTC ATACTCGGCGGTGGCA**AA**GGGACTCAGCTCTTCCCTCTCACAAG CACAAGGGCCACACCTGCTGTTCCTATTGGAGG	5977
	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTTGTGAGAGG GAAGAGCTGAGTCCC**TT**TGCCACCGCCGAGTATGACGGCCGCGA CCTCGTTCGGATCGGCGTAATTCCTGCGGAAGG	5978
	CGGTGGCA**AA**GGGACTC	5979
	GAGTCCC**TT**TGCCACCG	5980
Increased Starch ADPGPP *Triticum aestivum* Pro127Leu CCC-CTC	CAAGCACAAGGGCCACACCTGCTGTTCCTATTGGAGGATGTTACA GGCTCATCGATATTC**T**CATGAGCAACTGCTTCAATAGTGGCATCAA CAAGATATTCGTCATGACGCAGTTCAACTC	5981
	GAGTTGAACTGCGTCATGACGAATATCTTGTTGATGCCACTATTGA AGCAGTTGCTCATG**A**GAATATCGATGAGCCTGTAACATCCTCCAA TAGGAACAGCAGGTGTGGCCCTTGTGCTTG	5982
	CGATATTC**T**CATGAGCA	5983
	TGCTCATG**A**GAATATCG	5984
Increased Starch ADPGPP *Triticum aestivum* Gly162Asn GGA-AAT	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG**AAT**ATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5985
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGAT**ATT**CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	5986
	CGGCGGG**AAT**ATCAATT	5987
	AATTGAT**ATT**CCCGCCG	5988
Increased Starch ADPGPP *Triticum aestivum* Gly162Asn GGA-AAC	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG**AAC**ATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5989
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGAT**GTT**CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	5990
	CGGCGGG**AAC**ATCAATT	5991
	AATTGAT**GTT**CCCGCCG	5992
Increased Starch ADPGPP *Zea mays* Thr96Lys ACC-AAA	CTTTTCGGAGGAATTATGCTGATCCTAATGAAGTCGCTGCCGTCA TTTTGGGTGGTGGTA**AA**GGGACTCAGCTTTTCCCTCTCACAAGCA CAAGGGCCACCCCTGCTGTTCCTATTGGAGG	5993
	CCTCCAATAGGAACAGCAGGGGTGGCCCTTGTGCTTGTGAGAGG GAAAAGCTGAGTCCC**TT**TACCACCACCCAAAATGACGGCAGCGAC TTCATTAGGATCAGCATAATTCCTCCGAAAAG	5994
	TGGTGGTA**AA**GGGACTC	5995

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAGTCCCTTTACCACCA	5996
Increased Starch ADPGPP *Zea mays* Pro124Leu CCC-CTC	CAAGCACAAGGGCCACCCCTGCTGTTCCTATTGGAGGATGTTACAGGCTTATTGATATCCTCATGAGCAACTGTTTCAACAGTGGCATAAACAAGATATTTGTTATGACTCAGTTCAACTC	5997
	GAGTTGAACTGAGTCATAACAAATATCTTGTTTATGCCACTGTTGAAACAGTTGCTCATGAGGATATCAATAAGCCTGTAACATCCTCCAATAGGAACAGCAGGGGTGGCCCTTGTGCTTG	5998
	TGATATCCTCATGAGCA	5999
	TGCTCATGAGGATATCA	6000
Increased Starch ADPGPP *Zea mays* Gly159Asn GGG-AAT	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTACCTATCTTGGTGGG**AAT**ATCAACTTCACTGATGGATCTGTTGAGGTGCTGGCTGCAACACAAATGCCTGGGGAGGC	6001
	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCATCAGTGAAGTTGAT**ATT**CCCACCAAGATAGGTACGATGAATGTGACGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	6002
	TGGTGGG**AAT**ATCAACT	6003
	AGTTGAT**ATT**CCCACCA	6004
Increased Starch ADPGPP *Zea mays* Gly159Asn GGG-AAC	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTACCTATCTTGGTGGG**AAC**ATCAACTTCACTGATGGATCTGTTGAGGTGCTGGCTGCAACACAAATGCCTGGGGAGGC	6005
	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCATCAGTGAAGTTGAT**GTT**CCCACCAAGATAGGTACGATGAATGTGACGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	6006
	TGGTGGG**AAC**ATCAACT	6007
	AGTTGAT**GTT**CCCACCA	6008
Increased Starch ADPGPP *Solanum tuberosum* Ala58Lys GCG-AAG	CTTGAGAGGCAAAAGAAGGGCGATGCAAGGACAGTAGTAGCAATCATTCTAGGAGGGGGAAAGGGAACTCGTCTTTTCCCCCTCACCAAACGTCGTGCTAAGCCTGCCGTTCCAATGGGAG	6009
	CTCCCATTGGAACGGCAGGCTTAGCACGACGTTTGGTGAGGGGGAAAAGACGAGTTCCCTTTCCCCCTCCTAGAATGATTGCTACTACTGTCCTTGCATCGCCCTTCTTTTGCCTCTCAAG	6010
	GAGGGGGAAAGGGAACT	6011
	AGTTCCCTTTCCCCCTC	6012
Increased Starch ADPGPP *Solanum tuberosum* Pro86Leu CCA-CTA	CCAAACGTCGTGCTAAGCCTGCCGTTCCAATGGGAGGAGCATATAGGCTAATTGATGTACTAATGAGCAACTGTATTAACAGTGGCATCAACAAAGTATACATTCTCACTCAATTCAACTC	6013
	GAGTTGAATTGAGTGAGAATGTATACTTTGTTGATGCCACTGTTAATACAGTTGCTCATTAGTACATCAATTAGCCTATATGCTCCTCCCATTGGAACGGCAGGCTTAGCACGACGTTTGG	6014

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATGTACTAATGAGCA	6015
	TGCTCATTAGTACATCA	6016
Increased Starch ADPGPP *Solanum tuberosum* Gly122Asn GGG-AAT	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTACAACTTTGGCAAT**AAT**GTCACATTCGAGAGTGGCTATGTCGAGGTCTTAGCAGCAACTCAAACACCAGGTGAATT	6017
	AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCACTCTCGAATGTGAC**ATT**ATTGCCAAAGTTGTAAGCACGAGCTATATGCCTGTTAAGTGAGGCTGAGTTGAATTGAG	6018
	TGGCAAT**AAT**GTCACAT	6019
	ATGTGAC**ATT**ATTGCCA	6020
Increased Starch ADPGPP *Solanum tuberosum* Gly122Asn GGG-AAC	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTACAACTTTGGCAAT**AAC**GTCACATTCGAGAGTGGCTATGTCGAGGTCTTAGCAGCAACTCAAACACCAGGTGAATT	6021
	AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCACTCTCGAATGTGAC**GTT**ATTGCCAAAGTTGTAAGCACGAGCTATATGCCTGTTAAGTGAGGCTGAGTTGAATTGAG	6022
	TGGCAAT**AAC**GTCACAT	6023
	ATGTGAC**GTT**ATTGCCA	6024
Increased Starch ADPGPP *Beta vulgaris* Ala98Lys GCT-AAA	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGTGCTGGGTGGTGGT**AAA**GGGACTCGCCTCTTTCCTCTTACTAGCAGGAGAGCTAAGCCAGCAGTGCCAATTGGAGG	6025
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGAAAGAGGCGAGTCCC**TTT**ACCACCACCCAGCACAATTGCAGCCACATTTTTTGGGTCAGCTTTTGGAGATTCAAATA	6026
	TGGTGGT**AAA**GGGACTC	6027
	GAGTCCC**TTT**ACCACCA	6028
Increased Starch ADPGPP *Beta vulgaris* Ala98Lys GCT-AAC	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGTGCTGGGTGGTGGT**AAC**GGGACTCGCCTCTTTCCTCTTACTAGCAGGAGAGCTAAGCCAGCAGTGCCAATTGGAGG	6029
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGAAAGAGGCGAGTCCC**GTT**ACCACCACCCAGCACAATTGCAGCCACATTTTTTGGGTCAGCTTTTGGAGATTCAAATA	6030
	TGGTGGT**AAC**GGGACTC	6031
	GAGTCCC**GTT**ACCACCA	6032
Increased Starch ADPGPP *Beta vulgaris* Pro126Leu CCT-CTT	CTAGCAGGAGAGCTAAGCCAGCAGTGCCAATTGGAGGGTGTTACAGGCTGATTGATGTGCTTATGAGCAACTGCATCAACAGTGGCATTAGAAAGATTTTCATTCTTACCCAGTTCAATTC	6033

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAATTGAACTGGGTAAGAATGAAAATCTTTCTAATGCCACTGTTGA TGCAGTTGCTCATA**A**GCACATCAATCAGCCTGTAACACCCTCCAA TTGGCACTGCTGGCTTAGCTCTCCTGCTAG	6034
	TGATGTGC**T**TATGAGCA	6035
	TGCTCATA**A**GCACATCA	6036
Increased Starch ADPGPP *Beta vulgaris* Gly162Asn GGT-AAT	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTTGGAGAT**AAT**GTGAATTTTGGGGATGGCTTTGTGGAGGTT TTTGCTGCTACACAAACACCTGGAGAATC	6037
	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATTCAC**ATT**ATCTCCAAAATTATAGGTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG	6038
	TGGAGAT**AAT**GTGAATT	6039
	AATTCAC**ATT**ATCTCCA	6040
Increased Starch ADPGPP *Beta vulgaris* Gly162Asn GGT-AAC	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTTGGAGAT**AAC**GTGAATTTTGGGGATGGCTTTGTGGAGGT TTTTGCTGCTACACAAACACCTGGAGAATC	6041
	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATTCAC**GTT**ATCTCCAAAATTATAGGTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG	6042
	TGGAGAT**AAC**GTGAATT	6043
	AATTCAC**GTT**ATCTCCA	6044

Table 21
Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Arabidopsis thaliana* Ser12Term TCA-TGA	GAATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTTCTAACTTTGTGTGAAGAACTTCACTTTTCAACAATCATGGTGCTTCTTCATGCTCTGATGTCGCTCAGATTAC	6045
	GTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTGAAAAGTGAAGTTCTTCACACAAAGTTAGAAGAAGCAGTCACAGTTGCCATTATGAACTACCCGTTTACCTGGATTC	6046
	CTTTGTGTGAAGAACTT	6047
	AAGTTCTTCACACAAAG	6048
Waxy starch GBSS *Arabidopsis thaliana* Arg13Term AGA-TGA	ATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTTCTAACTTTGTGTCATGAACTTCACTTTTCAACAATCATGGTGCTTCTTCATGCTCTGATGTCGCTCAGATTACCT	6049
	AGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTGAAAAGTGAAGTTCATGACACAAAGTTAGAAGAAGCAGTCACAGTTGCCATTATGAACTACCCGTTTACCTGGAT	6050
	TTGTGTCATGAACTTCA	6051
	TGAAGTTCATGACACAA	6052
Waxy starch GBSS *Arabidopsis thaliana* Ser15Term TCA-TGA	TAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTTCTAACTTTGTGTCAAGAACTTGACTTTTCAACAATCATGGTGCTTCTTCATGCTCTGATGTCGCTCAGATTACCTTAAAAGG	6053
	CCTTTTAAGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTGAAAAGTCAAGTTCTTGACACAAAGTTAGAAGAAGCAGTCACAGTTGCCATTATGAACTACCCGTTTA	6054
	AAGAACTTGACTTTTCA	6055
	TGAAAAGTCAAGTTCTT	6056
Waxy starch GBSS *Arabidopsis thaliana* Ser24Term TCA-TGA	TGACTGCTTCTTCTAACTTTGTGTCAAGAACTTCACTTTTCAACAATCATGGTGCTTCTTGATGCTCTGATGTCGCTCAGATTACCTTAAAAGGCCAATCCTTGACTCATTGTGGGTTAAG	6057
	CTTAACCCACAATGAGTCAAGGATTGGCCTTTTAAGGTAATCTGAGCGACATCAGAGCATCAAGAAGCACCATGATTGTTGAAAAGTGAAGTTCTTGACACAAAGTTAGAAGAAGCAGTCA	6058
	TGCTTCTTGATGCTCTG	6059
	CAGAGCATCAAGAAGCA	6060

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Arabidopsis thaliana* Cys25Term TGC-TGA	TGCTTCTTCTAACTTTGTGTCAAGAACTTCACTTTTCAACAATCATGGTGCTTCTTCATG**A**TCTGATGTCGCTCAGATTACCTTAAAAGGCCAATCCTTGACTCATTGTGGGTTAAGGTCA	6061
	TGACCTTAACCCACAATGAGTCAAGGATTGGCCTTTTAAGGTAATCTGAGCGACATCAGA**T**CATGAAGAAGCACCATGATTGTTGAAAAGTGAAGTTCTTGACACAAAGTTAGAAGAAGCA	6062
	TCTTCATG**A**TCTGATGT	6063
	ACATCAGA**T**CATGAAGA	6064
Waxy starch GBSS *Antirrhinum majus* Lys24Term AAA-TAA	GTAACAGCTTCACAGTTGGTGTCACATGTCCATGGTGGAGCAACGTCTTCACCGGATACT**T**AAACAAACTTGGCCCAGGTTGGCCTCAGGAACCAGCAATTCACTCACAATGGGTTGAGAT	6065
	ATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGAGGCCAACCTGGGCCAAGTTTGTTT**A**AGTATCCGGTGAAGACGTTGCTCCACCATGGACATGTGACACCAACTGTGAAGCTGTTAC	6066
	CGGATACT**T**AAACAAAC	6067
	GTTTGTTT**A**AGTATCCG	6068
Waxy starch GBSS *Antirrhinum majus* Leu27Term TTG-TAG	CACAGTTGGTGTCACATGTCCATGGTGGAGCAACGTCTTCACCGGATACTAAAACAAACT**A**GGCCCAGGTTGGCCTCAGGAACCAGCAATTCACTCACAATGGGTTGAGATCAATAAACAT	6069
	ATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGAGGCCAACCTGGGCC**T**AGTTTGTTTTAGTATCCGGTGAAGACGTTGCTCCACCATGGACATGTGACACCAACTGTG	6070
	AACAAACT**A**GGCCCAGG	6071
	CCTGGGCC**T**AGTTTGTT	6072
Waxy starch GBSS *Antirrhinum majus* Gln29Term CAG-TAG	TTGGTGTCACATGTCCATGGTGGAGCAACGTCTTCACCGGATACTAAAACAAACTTGGCC**T**AGGTTGGCCTCAGGAACCAGCAATTCACTCACAATGGGTTGAGATCAATAAACATGGTTG	6073
	CAACCATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGAGGCCAACCT**A**GGCCAAGTTTGTTTTAGTATCCGGTGAAGACGTTGCTCCACCATGGACATGTGACACCAA	6074
	ACTTGGCC**T**AGGTTGGC	6075
	GCCAACCT**A**GGCCAAGT	6076
Waxy starch GBSS *Antirrhinum majus* Gln35Term CAG-TAG	GGTGGAGCAACGTCTTCACCGGATACTAAAACAAACTTGGCCCAGGTTGGCCTCAGGAAC**T**AGCAATTCACTCACAATGGGTTGAGATCAATAAACATGGTTGATAAGCTTCAAATGAGGA	6077
	TCCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCT**A**GTTCCTGAGGCCAACCTGGGCCAAGTTTGTTTTAGTATCCGGTGAAGACGTTGCTCCACC	6078

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCAGGAACTAGCAATTC	6079
	GAATTGCTAGTTCCTGA	6080
Waxy starch GBSS *Antirrhinum majus* Gln36Term CAA-TAA	GGAGCAACGTCTTCACCGGATACTAAAACAAACTTGGCCCAGGTTGGCCTCAGGAACCAGTAATTCACTCACAATGGGTTGAGATCAATAAACATGGTTGATAAGCTTCAAATGAGGAACA	6081
	TGTTCCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCATTGTGAGTGAATTACTGGTTCCTGAGGCCAACCTGGGCCAAGTTTGTTTTAGTATCCGGTGAAGACGTTGCTCC	6082
	GGAACCAGTAATTCACT	6083
	AGTGAATTACTGGTTCC	6084
Waxy starch GBSS *Ipomoea batatas* Gly20Term GGA-TGA	GTGATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTTGAGAATCAAAAGTGGGGTTGGGTCAATTAGCCCTGAGGAGCCAAGCTGTGACTCACAATG	6085
	CATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACCCCACTTTTGATTCTCAAGAAGTGGCACCCCCACAGACATGAGAAACAAAGTGTGAGGCAGTTATAGTCGCCATCAC	6086
	CCACTTCTTGAGAATCA	6087
	TGATTCTCAAGAAGTGG	6088
Waxy starch GBSS *Ipomoea batatas* Glu21Term GAA-TAA	ATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGATAATCAAAAGTGGGGTTGGGTCAATTAGCCCTGAGGAGCCAAGCTGTGACTCACAATGGGT	6089
	ACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACCCCACTTTTGATTATCCAGAAGTGGCACCCCCACAGACATGAGAAACAAAGTGTGAGGCAGTTATAGTCGCCAT	6090
	CTTCTGGATAATCAAAA	6091
	TTTTGATTATCCAGAAG	6092
Waxy starch GBSS *Ipomoea batatas* Ser22Term TCA-TGA	CGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGAGAATGAAAAGTGGGGTTGGGTCAATTAGCCCTGAGGAGCCAAGCTGTGACTCACAATGGGTTGAG	6093
	CTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACCCCACTTTTCATTCTCCAGAAGTGGCACCCCCACAGACATGAGAAACAAAGTGTGAGGCAGTTATAGTCG	6094
	TGGAGAATGAAAAGTGG	6095
	CCACTTTTCATTCTCCA	6096

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Ipomoea batatas* Lys23Term AAA-TAA	ACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCA CTTCTGGAGAATCATAAGTGGGGTTGGGTCAATTAGCCCTGAGGA GCCAAGCTGTGACTCACAATGGGTTGAGAC	6097
	GTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATT GACCCAACCCCACTTATGATTCTCCAGAAGTGGCACCCCCACAGA CATGAGAAACAAAGTGTGAGGCAGTTATAGT	6098
	GAGAATCATAAGTGGGG	6099
	CCCCACTTATGATTCTC	6100
Waxy starch GBSS *Ipomoea batatas* Leu26Term TTG-TAG	CCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGAGA ATCAAAAGTGGGGTAGGGTCAATTAGCCCTGAGGAGCCAAGCTGT GACTCACAATGGGTTGAGACCTGTGAACAA	6101
	TTGTTCACAGGTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCA GGGCTAATTGACCCTACCCCACTTTTGATTCTCCAGAAGTGGCAC CCCCACAGACATGAGAAACAAAGTGTGAGG	6102
	AGTGGGGTAGGGTCAAT	6103
	ATTGACCCTACCCCACT	6104
Waxy starch GBSS *Astragalus membranaeus* Tyr8Term TAT-TAG	CATCGGCGATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAAC GGTGACGGGGTCTTAGGTGGTGTCGAGAAGCGCGTGCTTCAATTC CCAGGGAAGAACAGAAGCCAAAGTGAATTCA	6105
	TGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATTGAAGCACGCG CTTCTCGACACCACCTAAGACCCCGTCACCGTTGCCATTCTGTGA GAGAGCAGTAAGGAGCAACAATCGCCGATG	6106
	GGGTCTTAGGTGGTGTC	6107
	GACACCACCTAAGACCC	6108
Waxy starch GBSS *Astragalus membranaeus* Ser11Term TCG-TAG	ATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGG GGTCTTATGTGGTGTAGAGAAGCGCGTGCTTCAATTCCCAGGGAA GAACAGAAGCCAAAGTGAATTCACCTCAGAA	6109
	TTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATTGA AGCACGCGCTTCTCTACACCACATAAGACCCCGTCACCGTTGCCA TTCTGTGAGAGAGCAGTAAGGAGCAACAAT	6110
	TGTGGTGTAGAGAAGCG	6111
	CGCTTCTCTACACCACA	6112

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Astragalus membranaeus* Arg12Term AGA-TGA	TGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGGGGTCTTATGTGGTGTCGTGAAGCGCGTGCTTCAATTCCCAGGGAAGAACAGAAGCCAAAGTGAATTCACCTCAGAAGA	6113
	TCTTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATTGAAGCACGCGCTTCACGACACCACATAAGACCCCGTCACCGTTGCCATTCTGTGAGAGAGCAGTAAGGAGCAACA	6114
	TGGTGTCGTGAAGCGCG	6115
	CGCGCTTCACGACACCA	6116
Waxy starch GBSS *Astragalus membranaeus* Cys15Term TGC-TGA	ACTGCTCTCTCACAGAATGGCAACGGTGACGGGGTCTTATGTGGTGTCGAGAAGCGCGTGATTCAATTCCCAGGGAAGAACAGAAGCCAAAGTGAATTCACCTCAGAAGATAAATCTCAAT	6117
	ATTGAGATTTATCTTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATTGAATCACGCGCTTCTCGACACCACATAAGACCCCGTCACCGTTGCCATTCTGTGAGAGAGCAGT	6118
	AGCGCGTGATTCAATTC	6119
	GAATTGAATCACGCGCT	6120
Waxy starch GBSS *Astragalus membranaeus* Gln19Term CAG-TAG	CACAGAATGGCAACGGTGACGGGGTCTTATGTGGTGTCGAGAAGCGCGTGCTTCAATTCCTAGGGAAGAACAGAAGCCAAAGTGAATTCACCTCAGAAGATAAATCTCAATAGCCAAGCAT	6121
	ATGCTTGGCTATTGAGATTTATCTTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTCCCTAGGAATTGAAGCACGCGCTTCTCGACACCACATAAGACCCCGTCACCGTTGCCATTCTGTG	6122
	TCAATTCCTAGGGAAGA	6123
	TCTTCCCTAGGAATTGA	6124
Waxy starch GBSS *Solanum tuberosum* Ser7Term TCA-TGA	TGTAGCTTGGTAGATTCCCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTGACACCACTTTGTGTCAAGAAGCCAAACTTCACTAGACACCAAATCAACCTTGTCACAGAT	6125
	ATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTTGGCTTCTTGACACAAAGTGGTGTCAAGCTGTGATGCTTGCCATGTGATGTGTGGTCTACAAAAAGGGGAATCTACCAAGCTACA	6126
	CACAGCTTGACACCACT	6127
	AGTGGTGTCAAGCTGTG	6128
Waxy starch GBSS *Solanum tuberosum* Ser12Term TCA-TGA	TCCCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTGAAGAAGCCAAACTTCACTAGACACCAAATCAACCTTGTCACAGATAGGACTCAGGAACCA	6129
	TGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTTGGCTTCTTCACACAAAGTGGTGTGAAGCTGTGATGCTTGCCATGTGATGTGTGGTCTACAAAAAGGGGA	6130

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTTTGTGT**G**AAGAAGCC	6131
	GGCTTCTT**C**ACACAAAG	6132
Waxy starch GBSS *Solanum tuberosum* Arg13Term AGA-TGA	CCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTCA**T**GAAGCCAAACTTCACTAGACACCAAATCAACCTTGTCACAGATAGGACTCAGGAACCATA	6133
	TATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTTGGCTTC**A**TGACACAAAGTGGTGTGAAGCTGTGATGCTTGCCATGTGATGTGTGGTCTACAAAAAGGG	6134
	TTGTGTCA**T**GAAGCCAA	6135
	TTGGCTTC**A**TGACACAA	6136
Waxy starch GBSS *Solanum tuberosum* Gln15Term CAA-TAA	TTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTCAAGAAGC**T**AAACTTCACTAGACACCAAATCAACCTTGTCACAGATAGGACTCAGGAACCATACTCTGA	6137
	TCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTT**A**GCTTCTTGACACAAAGTGGTGTGAAGCTGTGATGCTTGCCATGTGATGTGTGGTCTACAA	6138
	CAAGAAGC**T**AAACTTCA	6139
	TGAAGTTT**A**GCTTCTTG	6140
Waxy starch GBSS *Solanum tuberosum* Ser17Term TCA-TGA	CCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTCAAGAAGCCAAACTT**G**ACTAGACACCAAATCAACCTTGTCACAGATAGGACTCAGGAACCATACTCTGACTCACAA	6141
	TTGTGAGTCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGT**C**AAGTTTGGCTTCTTGACACAAAGTGGTGTGAAGCTGTGATGCTTGCCATGTGATGTGTGG	6142
	CCAAACTT**G**ACTAGACA	6143
	TGTCTAGT**C**AAGTTTGG	6144
Waxy starch GBSS *Pisum sativum* Gly6Term GGA-TGA	GTCGATCACTCTTCTCTCACCGCCGAAACAGATTTTGACACAAAAATGGCAACAATAACG**T**GATCTTCAATGCCGACGAGAACCGCGTGCTTCAATTACCAAGGAAGATCAGCAGAGTCTA	6145
	TAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGGTTCTCGTCGGCATTGAAGATC**A**CGTTATTGTTGCCATTTTTGTGTCAAAATCTGTTTCGGCGGTGAGAGAAGAGTGATCGAC	6146
	CAATAACG**T**GATCTTCA	6147
	TGAAGATC**A**CGTTATTG	6148

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Pisum sativum* Ser8Term TCA-TGA	ACTCTTCTCTCACCGCCGAAACAGATTTTGACACAAAAATGGCAACAATAACGGGATCTTGAATGCCGACGAGAACCGCGTGCTTCAATTACCAAGGAAGATCAGCAGAGTCTAAACTGAA	6149
	TTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGGTTCTCGTCGGCATTCAAGATCCCGTTATTGTTGCCATTTTTGTGTCAAAATCTGTTTCGGCGGTGAGAGAAGAGT	6150
	GGGATCTTGAATGCCGA	6151
	TCGGCATTCAAGATCCC	6152
Waxy starch GBSS *Pisum sativum* Arg12Term AGA-TGA	ACCGCCGAAACAGATTTTGACACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACGTGAACCGCGTGCTTCAATTACCAAGGAAGATCAGCAGAGTCTAAACTGAATTTGCCTCAGA	6153
	TCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGGTTCACGTCGGCATTGAAGATCCCGTTATTGTTGCCATTTTTGTGTCAAAATCTGTTTCGGCGGT	6154
	TGCCGACGTGAACCGCG	6155
	CGCGGTTCACGTCGGCA	6156
Waxy starch GBSS *Pisum sativum* Cys15Term TGC-TGA	AGATTTTGACACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACGAGAACCGCGTGATTCAATTACCAAGGAAGATCAGCAGAGTCTAAACTGAATTTGCCTCAGATACACTTCAAT	6157
	ATTGAAGTGTATCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATTGAATCACGCGGTTCTCGTCGGCATTGAAGATCCCGTTATTGTTGCCATTTTTGTGTCAAAATCT	6158
	ACCGCGTGATTCAATTA	6159
	TAATTGAATCACGCGGT	6160
Waxy starch GBSS *Pisum sativum* Tyr18Term TAC-TAG	CACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACGAGAACCGCGTGCTTCAATTAGCAAGGAAGATCAGCAGAGTCTAAACTGAATTTGCCTCAGATACACTTCAATAACAACCAA	6161
	TTGGTTGTTATTGAAGTGTATCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTTCCTTGCTAATTGAAGCACGCGGTTCTCGTCGGCATTGAAGATCCCGTTATTGTTGCCATTTTTGTG	6162
	TTCAATTAGCAAGGAAG	6163
	CTTCCTTGCTAATTGAA	6164
Waxy starch GBSS *Manihot esculenta* Ser14Term TCA-TGA	TCTACACCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTCGTTTCCAGGAGCTGACACTTGAGCATCCATGCATTAGAGACTAAGGCTAATAATTTGTCTCACACTGGACCCTG	6165
	CAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTAATGCATGGATGCTCAAGTGTCAGCTCCTGGAAACGAAATGTGCAGCTATTACAGTTGCCATGGTGCTCTCTCCGGTGTAGA	6166

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAGGAGCTGACACTTGA	6167
	TCAAGTGTCAGCTCCTG	6168
Waxy starch GBSS *Manihot esculenta* Leu16Term TTG-TAG	CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACTAGAGCATCCATGCATTAGAGACTAAGGCTAATAATTTGTCTCACACTGGACCCTGGACCCA	6169
	TGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTAATGCATGGATGCTCTAGTGTGAGCTCCTGGAAACGAAATGTGCAGCTATTACAGTTGCCATGGTGCTCTCTCCGG	6170
	CTCACACTAGAGCATCC	6171
	GGATGCTCTAGTGTGAG	6172
Waxy starch GBSS *Manihot esculenta* Leu21Term TTA-TGA	TGGCAACTGTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACTTGAGCATCCATGCATGAGAGACTAAGGCTAATAATTTGTCTCACACTGGACCCTGGACCCAAACTATCACTCCCAA	6173
	TTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTCATGCATGGATGCTCAAGTGTGAGCTCCTGGAAACGAAATGTGCAGCTATTACAGTTGCCA	6174
	CCATGCATGAGAGACTA	6175
	TAGTCTCTCATGCATGG	6176
Waxy starch GBSS *Manihot esculenta* Glu22Term GAG-TAG	GCAACTGTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACTTGAGCATCCATGCATTATAGACTAAGGCTAATAATTTGTCTCACACTGGACCCTGGACCCAAACTATCACTCCCAATG	6177
	CATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTATAATGCATGGATGCTCAAGTGTGAGCTCCTGGAAACGAAATGTGCAGCTATTACAGTTGC	6178
	ATGCATTATAGACTAAG	6179
	CTTAGTCTATAATGCAT	6180
Waxy starch GBSS *Manihot esculenta* Lys24Term AAG-TAG	GTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACTTGAGCATCCATGCATTAGAGACTTAGGCTAATAATTTGTCTCACACTGGACCCTGGACCCAAACTATCACTCCCAATGGTTTAA	6181
	TTAAACCATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTAAGTCTCTAATGCATGGATGCTCAAGTGTGAGCTCCTGGAAACGAAATGTGCAGCTATTAC	6182
	TAGAGACTTAGGCTAAT	6183
	ATTAGCCTAAGTCTCTA	6184

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Phaseolus vulgaris* Ser12Term TCA-TGA	ACAACTCCTCCGTCACCGGTATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGCGT**G**AAAAGGCGCGTGGAGTACAGAGACAAAAGTGAAATCTTCGGGTCAGATGAGCCTGAACCG	6185
	CGGTTCAGGCTCATCTGACCCGAAGATTTCACTTTTGTCTCTGTACTCCACGCGCCTTTT**C**ACGCCACGCACGATGCCATCGATACCGTTGCCATGCTTATACCGGTGACGGAGGAGTTGT	6186
	CGTGGCGT**G**AAAAGGCG	6187
	CGCCTTTT**C**ACGCCACG	6188
Waxy starch GBSS *Phaseolus vulgaris* Trp16Term TGG-TGA	CACCGGTATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTG**A**AGTACAGAGACAAAAGTGAAATCTTCGGGTCAGATGAGCCTGAACCGTCATGAATTGAAA	6189
	TTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATTTCACTTTTGTCTCTGTACT**T**CACGCGCCTTTTGACGCCACGCACGATGCCATCGATACCGTTGCCATGCTTATACCGGTG	6190
	GGCGCGTG**A**AGTACAGA	6191
	TCTGTACT**T**CACGCGCC	6192
Waxy starch GBSS *Phaseolus vulgaris* Glu19Term GAG-TAG	ATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTGGAGTACA**T**AGACAAAAGTGAAATCTTCGGGTCAGATGAGCCTGAACCGTCATGAATTGAAATACGATG	6193
	CATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATTTCACTTTTGTCT**A**TGTACTCCACGCGCCTTTTGACGCCACGCACGATGCCATCGATACCGTTGCCATGCTTAT	6194
	GGAGTACA**T**AGACAAAA	6195
	TTTTGTCT**A**TGTACTCC	6196
Waxy starch GBSS *Phaseolus vulgaris* Lys21Term AAA-TAA	ATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTGGAGTACAGAGACA**T**AAGTGAAATCTTCGGGTCAGATGAGCCTGAACCGTCATGAATTGAAATACGATGGGTTGA	6197
	TCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATTTCACTT**A**TGTCTCTGTACTCCACGCGCCTTTTGACGCCACGCACGATGCCATCGATACCGTTGCCAT	6198
	CAGAGACA**T**AAGTGAAA	6199
	TTTCACTT**A**TGTCTCTG	6200
Waxy starch GBSS *Phaseolus vulgaris* Lys23Term AAA-TAA	ACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTGGAGTACAGAGACAAAAGTG**T**AATCTTCGGGTCAGATGAGCCTGAACCGTCATGAATTGAAATACGATGGGTTGAGATCTC	6201
	GAGATCTCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATT**A**CACTTTTGTCTCTGTACTCCACGCGCCTTTTGACGCCACGCACGATGCCATCGATACCGT	6202

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAAAAGTGTAATCTTCG	6203
	CGAAGATTACACTTTTG	6204
Waxy starch GBSS *Triticum aestivum* Tyr7Term TAT-TAG	GCGCCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGG GTTCCATTCCTAATTAGTGTTCTTATCAAACAAACAGTGTTGGTTCA CTGAAACTGTCGCCTCACATCCAATTCCAG	6205
	CTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACTGTTT GTTTGATAAGAACACTAATTAGGAATGGAACCCATTGGTGCAGCCT CTCAATGACGACCTTTTCGAGCTAGGCGC	6206
	CCTAATTAGTGTTCTTA	6207
	TAAGAACACTAATTAGG	6208
Waxy starch GBSS *Triticum aestivum* Cys8Term TGT-TGA	CCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTC CATTCCTAATTATTGATCTTATCAAACAAACAGTGTTGGTTCACTGA AACTGTCGCCTCACATCCAATTCCAGCAA	6209
	TTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACT GTTTGTTTGATAAGATCAATAATTAGGAATGGAACCCATTGGTGCA GCCTCTCAATGACGACCTTTTCGAGCTAGG	6210
	AATTATTGATCTTATCA	6211
	TGATAAGATCAATAATT	6212
Waxy starch GBSS *Triticum aestivum* Tyr10Term TAT-TAG	TCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCC TAATTATTGTTCTTAGCAAACAAACAGTGTTGGTTCACTGAAACTGT CGCCTCACATCCAATTCCAGCAATCTTGT	6213
	ACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACC AACACTGTTTGTTTGCTAAGAACAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTTCGA	6214
	TGTTCTTAGCAAACAAA	6215
	TTTGTTTGCTAAGAACA	6216
Waxy starch GBSS *Triticum aestivum* Gln11Term CAA-TAA	CGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCCT AATTATTGTTCTTATTAAACAAACAGTGTTGGTTCACTGAAACTGTC GCCTCACATCCAATTCCAGCAATCTTGTA	6217
	TACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAAC CAACACTGTTTGTTTAATAAGAACAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTTCG	6218
	GTTCTTATTAAACAAAC	6219
	GTTTGTTTAATAAGAAC	6220

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Triticum aestivum* Ser17Term TCA-TGA	AGGCTGCACCAATGGGTTCCATTCCTAATTATTGTTCTTATCAAACAAACAGTGTTGGTTGACTGAAACTGTCGCCTCACATCCAATTCCAGCAATCTTGTAACAATGAAGTTATGTTCCT	6221
	AGGAACATAACTTCATTGTTACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTCAACCAACACTGTTTGTTTGATAAGAACAATAATTAGGAATGGAACCCATTGGTGCAGCCT	6222
	TGTTGGTTGACTGAAAC	6223
	GTTTCAGTCAACCAACA	6224
Waxy starch GBSS *Triticum aestivum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTTCCGGCGTGCAGGTTTCTAGGGCGTGAGGCCCCGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTA	6225
	TAGCTCCGACGGTCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCGGGGCCTCACGCCCTAGAAACCTGCACGCCGGAACCTGTCGGTGATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6226
	CAGGTTTCTAGGGCGTG	6227
	CACGCCCTAGAAACCTG	6228
Waxy starch GBSS *Triticum aestivum* Gly46Term GGA-TGA	GGTTTCCAGGGCGTGAGGCCCCGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCTGAGCTAGCGCCGCCCCAACGCAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCT	6229
	AGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGCGTTGGGGCGGCGCTAGCTCAGACGGTCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	6230
	GGACCGTCTGAGCTAGC	6231
	GCTAGCTCAGACGGTCC	6232
Waxy starch GBSS *Triticum aestivum* Gln53Term CAA-TAA	CGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTAGCGCCGCCCCAACGTAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACCG	6233
	CGGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTACGTTGGGGCGGCGCTAGCTCCGACGGTCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCG	6234
	CCCCAACGTAAAGCCGG	6235
	CCGGCTTTACGTTGGGG	6236
Waxy starch GBSS *Triticum aestivum* Lys56Term AAA-TAA	GCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTAGCGCCGCCCCAACGCAAAGCCGGTAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCG	6237
	CGCCGCTGCCGGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTACCGGCTTTGCGTTGGGGCGGCGCTAGCTCCGACGGTCCTCATGCCGAGAGCCGCATCCGC	6238

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAGCCGGTAAGCGCAC	6239
	GTGCGCTTACCGGCTTT	6240
Waxy starch GBSS *Triticum aestivum* Glu85Term GAG-TAG	CTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCGGCATGAACCT CGTGTTCGTCGGCGCCTAGATGGCGCCCTGGAGCAAGACCGGCG GCCTCGGCGACGTCCTCGGGGGCCTCCCCCAG	6241
	CTGGGGGAGGCCCCCGAGGACGTCGCCGAGGCCGCCGGTCTT GCTCCAGGGCGCCATCTAGGCGCCGACGAACACGAGGTTCATGC CGCCGCTGCCGGTGGCGCGCACCACCATGGAGAG	6242
	TCGGCGCCTAGATGGCG	6243
	CGCCATCTAGGCGCCGA	6244
Waxy starch GBSS *Triticum aestivum* Gln8Term CAG-TAG	GTCGTCTCTCGCTGCAGGTAGCCACACCCTGCGCGCGCGATGGC GGCTCTGGTCACGTCGTAGCTCGCCACCTCCGGCACCGTCCTCG GCATCACCGACAGGTTCCGGCGTGCAGGTTTTC	6245
	GAAAACCTGCACGCCGGAACCTGTCGGTGATGCCGAGGACGGTG CCGGAGGTGGCGAGCTACGACGTGACCAGAGCCGCCATCGCGC GCGCAGGGTGTGGCTACCTGCAGCGAGAGACGAC	6246
	TCACGTCGTAGCTCGCC	6247
	GGCGAGCTACGACGTGA	6248
Waxy starch GBSS *Triticum aestivum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTTTAGGGTGTGAGGCCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6249
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACACCCTAAAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6250
	CAGGTTTTTAGGGTGTG	6251
	CACACCCTAAAAACCTG	6252
Waxy starch GBSS *Triticum aestivum* Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCG GAGCGAGCGCCGCCCCGTAGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG	6253
	CGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCTACGGGGCGGCGCTCGCTCCGGTAGTCC TCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6254
	CCGCCCCGTAGCAACAA	6255
	TTGTTGCTACGGGGCGG	6256

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Triticum aestivum* Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCCGAAGTAACAAAGCCGGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6257
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGGTAG TCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6258
	CCCCGAAGTAACAAAGC	6259
	GCTTTGTTACTTCGGGG	6260
Waxy starch GBSS *Triticum aestivum* Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA GCGCCGCCCCGAAGCAATAAAGCCGGAAAGCGCACCGCGGGAC CCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6261
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGG TAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6262
	CGAAGCAATAAAGCCGG	6263
	CCGGCTTTATTGCTTCG	6264
Waxy starch GBSS *Triticum durum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTCTAGGGCGTGAGGCCCCGGAACCCGGCG GATGCGGCCCTCGTCATGAGGACTATCGGAGCGA	6265
	TCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGCCGGGTTC CGGGGCCTCACGCCCTAGAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6266
	CAGGTTTCTAGGGCGTG	6267
	CACGCCCTAGAAACCTG	6268
Waxy starch GBSS *Triticum durum* Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGG AGCGAGCGCCGCCCCGTAGCAAAGCCGGAAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6269
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGCTCCCGCGGTG CGCTTTCCGGCTTTGCTACGGGGCGGCGCTCGCTCCGATAGTCC TCATGACGAGGGCCGCATCCGCCGGGTTCCGGGG	6270
	CCGCCCCGTAGCAAAGC	6271
	GCTTTGCTACGGGGCGG	6272
Waxy starch GBSS *Triticum durum* Gln53Term CAA-TAA	CGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGC GAGCGCCGCCCCGAAGTAAAGCCGGAAAGCGCACCGCGGGAGC CGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6273
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGCTCCCGCG GTGCGCTTTCCGGCTTTACTTCGGGGCGGCGCTCGCTCCGATAG TCCTCATGACGAGGGCCGCATCCGCCGGGTTCCG	6274

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCCCGAAG**T**AAAGCCGG	6275
	CCGGCTTT**A**CTTCGGGG	6276
Waxy starch GBSS *Triticum durum* Lys56Term AAA-TAA	GCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGCCCCGAAGCAAAGCCGG**T**AAGCGCACCGCGGGAGCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGGGCAGCGGCG	6277
	CGCCGCTGCCCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGCTCCCGCGGTGCGCTT**A**CCGGCTTTGCTTCGGGGCGGCGCTCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGC	6278
	AAAGCCGG**T**AAGCGCAC	6279
	GTGCGCTT**A**CCGGCTTT	6280
Waxy starch GBSS *Triticum durum* Cys64Term TGC-TGA	TATCGGAGCGAGCGCCGCCCCGAAGCAAAGCCGGAAAGCGCACCGCGGGAGCCGGCGGTG**A**CTCTCCATGGTGGTGCGCGCCACGGGCAGCGGCGGCATGAACCTCGTGTTCGTCGGCGCC	6281
	GGCGCCGACGAACACGAGGTTCATGCCGCCGCTGCCCGTGGCGCGCACCACCATGGAGAG**T**CACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTTGCTTCGGGGCGGCGCTCGCTCCGATA	6282
	CGGCGGTG**A**CTCTCCAT	6283
	ATGGAGAG**T**CACCGCCG	6284
Waxy starch GBSS *Triticum turgidum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTTCCGGCGTGCAGGTTTT**T**AGGGTGTGAGGCCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6285
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGGCCTCACACCCT**A**AAAACCTGCACGCCGGAACCTGTCGGTGATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6286
	CAGGTTTT**T**AGGGTGTG	6287
	CACACCCT**A**AAAACCTG	6288
Waxy starch GBSS *Triticum turgidum* Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCCG**T**AGCAACAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG	6289
	CGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTGCT**A**CGGGGCGGCGCTCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6290
	CCGCCCCG**T**AGCAACAA	6291
	TTGTTGCT**A**CGGGGCGG	6292

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Triticum turgidum* Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCCGAAGTAACAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6293
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6294
	CCCCGAAGTAACAAAGC	6295
	GCTTTGTTACTTCGGGG	6296
Waxy starch GBSS *Triticum turgidum* Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCCGAAGCAATAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6297
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6298
	CGAAGCAATAAAGCCGG	6299
	CCGGCTTTATTGCTTCG	6300
Waxy starch GBSS *Triticum turgidum* Lys57Term AAA-TAA	GATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCCGAAGCAACAAAGCCGGTAAGCGCACCGCGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGGGCAGCGCCG	6301
	CGGCGCTGCCCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTACCGGCTTTGTTGCTTCGGGGCGGCGCTCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATC	6302
	AAAGCCGGTAAGCGCAC	6303
	GTGCGCTTACCGGCTTT	6304
Waxy starch GBSS *Aegilops speltoides* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGCCACCGTCCTCGGCATCACCGACAGGTTCCGCCATGCAGGTTTCTAGGGCGTGAGGCCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAGCGA	6305
	TCGCTCCGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGGCCTCACGCCCTAGAAACCTGCATGGCGGAACCTGTCGGTGATGCCGAGGACGGTGGCGGAGGTGGCGAGCTG	6306
	CAGGTTTCTAGGGCGTG	6307
	CACGCCCTAGAAACCTG	6308
Waxy starch GBSS *Aegilops speltoides* Gly46Term GGA-TGA	GGTTTCCAGGGCGTGAGGCCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCTGAGCGAGCGCCGCCCCGAAGCAACAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCC	6309
	GGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTGCTTCGGGGCGGCGCTCGCTCAGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	6310

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGACTGTCTGAGCGAGC	6311
	GCTCGCTCAGACAGTCC	6312
Waxy starch GBSS *Aegilops speltoides* Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAGCGAGCGCCGCCCCGTAGCAACAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCGATGGTGGTGCGCG	6313
	CGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTGCTACGGGGCGGCGCTCGCTCCGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6314
	CCGCCCCGTAGCAACAA	6315
	TTGTTGCTACGGGGCGG	6316
Waxy starch GBSS *Aegilops speltoides* Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAGCGAGCGCCGCCCCGAAGTAACAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCGATGGTGGTGCGCGCCA	6317
	TGGCGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6318
	CCCCGAAGTAACAAAGC	6319
	GCTTTGTTACTTCGGGG	6320
Waxy starch GBSS *Aegilops speltoides* Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAGCGAGCGCCGCCCCGAAGCAATAAAGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCTCGATGGTGGTGCGCGCCACCG	6321
	CGGTGGCGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6322
	CGAAGCAATAAAGCCGG	6323
	CCGGCTTTATTGCTTCG	6324
Waxy starch GBSS *Oryza glaberrima* Gln8Term CAG-TAG	AGTGCAGAGATCTTCCACAGCAACAGCTAGACAACCACCATGTCGGCTCTCACCACGTCCTAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCTGACAGGTCGGCGCCGTCGTCGCTGC	6325
	GCAGCGACGACGGCGCCGACCTGTCAGCGATGCCGAAGCCGGTGGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGAAGATCTCTGCACT	6326
	CCACGTCCTAGCTCGCC	6327
	GGCGAGCTAGGACGTGG	6328

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Oryza glaberrima* Ser12Term TCG-TAG	TCCACAGCAACAGCTAGACAACCACCATGTCGGCTCTCACCACGT CCCAGCTCGCCACCT**A**GGCCACCGGCTTCGGCATCGCTGACAGG TCGGCGCCGTCGTCGCTGCTCCGCCACGGGTT	6329
	AACCCGTGGCGGAGCAGCGACGACGGCGCCGACCTGTCAGCGAT GCCGAAGCCGGTGGCC**T**AGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGA	6330
	CGCCACCT**A**GGCCACCG	6331
	CGGTGGCC**T**AGGTGGCG	6332
Waxy starch GBSS *Oryza glaberrima* Ser22Term TCG-TAG	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCTGACAGGT**A**GGCGCCGTCGTCGCTGCTCCGCCACGG GTTCCAGGGCCTCAAGCCCCGCAGCCCCGCCGG	6333
	CCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACCCGTGGCGGA GCAGCGACGACGGCGCC**T**ACCTGTCAGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6334
	TGACAGGT**A**GGCGCCGT	6335
	ACGGCGCC**T**ACCTGTCA	6336
Waxy starch GBSS *Oryza glaberrima* Ser25Term TCG-TAG	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCT GACAGGTCGGCGCCGT**A**GTCGCTGCTCCGCCACGGGTTCCAGG GCCTCAAGCCCCGCAGCCCCGCCGGCGGCGACGC	6337
	GCGTCGCCGCCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACC CGTGGCGGAGCAGCGAC**T**ACGGCGCCGACCTGTCAGCGATGCC GAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	6338
	GGCGCCGT**A**GTCGCTGC	6339
	GCAGCGAC**T**ACGGCGCC	6340
Waxy starch GBSS *Oryza glaberrima* Ser26Term TCG-TAG	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCTGAC AGGTCGGCGCCGTCGT**A**GCTGCTCCGCCACGGGTTCCAGGGCCT CAAGCCCCGCAGCCCCGCCGGCGGCGACGCGAC	6341
	GTCGCGTCGCCGCCGGCGGGGCTGCGGGGCTTGAGGCCCTGGA ACCCGTGGCGGAGCAGC**T**ACGACGGCGCCGACCTGTCAGCGATG CCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	6342
	GCCGTCGT**A**GCTGCTCC	6343
	GGAGCAGC**T**ACGACGGC	6344
Waxy starch GBSS *Oryza sativa* Gln8Term CAG-TAG	TCCACAGCAAGAGCTAAACAGCCGACCGTGTGCACCACCATGTCG GCTCTCACCACGTCC**T**AGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCCGACAGGTCGGCGCCGTCGTCGCTGC	6345
	GCAGCGACGACGGCGCCGACCTGTCGGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCT**A**GGACGTGGTGAGAGCCGACATGGTG GTGCACACGGTCGGCTGTTTAGCTCTTGCTGTGGA	6346

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCACGTCCTAGCTCGCC	6347
	GGCGAGCTAGGACGTGG	6348
Waxy starch GBSS *Oryza sativa* Ser12Term TCG-TAG	CTAAACAGCCGACCGTGTGCACCACCATGTCGGCTCTCACCACGTCCCAGCTCGCCACCTAGGCCACCGGCTTCGGCATCGCCGACAGGTCGGCGCCGTCGTCGCTGCTTCGCCACGGGTT	6349
	AACCCGTGGCGAAGCAGCGACGACGGCGCCGACCTGTCGGCGATGCCGAAGCCGGTGGCCTAGGTGGCGAGCTGGGACGTGGTGAGAGCCGACATGGTGGTGCACACGGTCGGCTGTTTAG	6350
	CGCCACCTAGGCCACCG	6351
	CGGTGGCCTAGGTGGCG	6352
Waxy starch GBSS *Oryza sativa* Ser22Term TCG-TAG	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCCGACAGGTAGGCGCCGTCGTCGCTGCTTCGCCACGGGTTCCAGGGCCTCAAGCCCCGTAGCCCAGCCGG	6353
	CCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCCGTGGCGAAGCAGCGACGACGGCGCCTACCTGTCGGCGATGCCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6354
	CGACAGGTAGGCGCCGT	6355
	ACGGCGCCTACCTGTCG	6356
Waxy starch GBSS *Oryza sativa* Ser25Term TCG-TAG	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCCGACAGGTCGGCGCCGTAGTCGCTGCTTCGCCACGGGTTCCAGGGCCTCAAGCCCCGTAGCCCAGCCGGCGGGGACGC	6357
	GCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCCGTGGCGAAGCAGCGACTACGGCGCCGACCTGTCGGCGATGCCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	6358
	GGCGCCGTAGTCGCTGC	6359
	GCAGCGACTACGGCGCC	6360
Waxy starch GBSS *Oryza sativa* Ser26Term TCG-TAG	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCCGACAGGTCGGCGCCGTCGTAGCTGCTTCGCCACGGGTTCCAGGGCCTCAAGCCCCGTAGCCCAGCCGGCGGGGACGCATC	6361
	GATGCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCCGTGGCGAAGCAGCTACGACGGCGCCGACCTGTCGGCGATGCCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	6362
	GCCGTCGTAGCTGCTTC	6363
	GAAGCAGCTACGACGGC	6364

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Hordeum vulgare* Gln8Term CAG-TAG	GTCTCTCACTGCAGGTAGCCACACCCTGTGCGCGGCGCCATGGC GGCTCTGGCCACGTCCTAGCTCGCCACCTCCGGCACCGTCCTCG GCGTCACCGACAGATTCCGGCGTCCAGGTTTTC	6365
	GAAAACCTGGACGCCGGAATCTGTCGGTGACGCCGAGGACGGTG CCGGAGGTGGCGAGCTAGGACGTGGCCAGAGCCGCCATGGCGC CGCGCACAGGGTGTGGCTACCTGCAGTGAGAGAC	6366
	CCACGTCCTAGCTCGCC	6367
	GGCGAGCTAGGACGTGG	6368
Waxy starch GBSS *Hordeum vulgare* Arg21Term AGA-TGA	ATGGCGGCTCTGGCCACGTCCCAGCTCGCCACCTCCGGCACCGT CCTCGGCGTCACCGACTGATTCCGGCGTCCAGGTTTTCAGGGCCT CAGGCCCCGGAACCCGGCGGATGCGGCGCTTG	6369
	CAAGCGCCGCATCCGCCGGGTTCCGGGGCCTGAGGCCCTGAAAA CCTGGACGCCGGAATCAGTCGGTGACGCCGAGGACGGTGCCGG AGGTGGCGAGCTGGGACGTGGCCAGAGCCGCCAT	6370
	TCACCGACTGATTCCGG	6371
	CCGGAATCAGTCGGTGA	6372
Waxy starch GBSS *Hordeum vulgare* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCGTCACCGACAGATT CCGGCGTCCAGGTTTTTAGGGCCTCAGGCCCCGGAACCCGGCGG ATGCGGCGCTTGGTATGAGGACTATCGGAGCAA	6373
	TTGCTCCGATAGTCCTCATACCAAGCGCCGCATCCGCCGGGTTCC GGGGCCTGAGGCCCTAAAAACCTGGACGCCGGAATCTGTCGGTG ACGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6374
	CAGGTTTTTAGGGCCTC	6375
	GAGGCCCTAAAAACCTG	6376
Waxy starch GBSS *Hordeum vulgare* Gly46Term GGA-TGA	GGTTTTCAGGGCCTCAGGCCCCGGAACCCGGCGGATGCGGCGCT TGGTATGAGGACTATCTGAGCAAGCGCCGCCCCGAAGCAAAGCC GGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCT	6377
	AGAGGCACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTTGCTTC GGGGCGGCGCTTGCTCAGATAGTCCTCATACCAAGCGCCGCATC CGCCGGGTTCCGGGGCCTGAGGCCCTGAAAACC	6378
	GGACTATCTGAGCAAGC	6379
	GCTTGCTCAGATAGTCC	6380
Waxy starch GBSS *Hordeum vulgare* Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCGGCGCTTGGTATGAGGACTATCGG AGCAAGCGCCGCCCCGTAGCAAAGCCGGAAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCGTGGTGGTGAGCGCCA	6381
	TGGCGCTCACCACCACGGAGAGGCACCGCCGGCTCCCGCGGTG CGCTTTCCGGCTTTGCTACGGGGCGGCGCTTGCTCCGATAGTCC TCATACCAAGCGCCGCATCCGCCGGGTTCCGGGG	6382

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGCCCCGTAGCAAAGC	6383
	GCTTTGCTACGGGGCGG	6384
Waxy starch GBSS *Zea mays* Gln8Term CAG-TAG	ACGTCTTTTCTCTCTCTCCTACGCAGTGGATTAATCGGCATGGCGGCTCTGGCCACGTCGTAGCTCGTCGCAACGCGCGCCGGCCTGGGCGTCCCGGACGCGTCCACGTTCCGCCGCGGCG	6385
	CGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCCAGGCCGGCGCGCGTTGCGACGAGCTACGACGTGGCCAGAGCCGCCATGCCGATTAATCCACTGCGTAGGAGAGAGAGAAAAGACGT	6386
	CCACGTCGTAGCTCGTC	6387
	GACGAGCTACGACGTGG	6388
Waxy starch GBSS *Zea mays* Gln30Term CAG-TAG	GTCGCAACGCGCGCCGGCCTGGGCGTCCCGGACGCGTCCACGTTCCGCCGCGGCGCCGCGTAGGGCCTGAGGGGGGCCCGGGCGTCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCG	6389
	CGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGACGCCCGGGCCCCCCTCAGGCCCTACGCGGCGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCCAGGCCGGCGCGCGTTGCGAC	6390
	GCGCCGCGTAGGGCCTG	6391
	CAGGCCCTACGCGGCGC	6392
Waxy starch GBSS *Zea mays* Ser38Term TCG-TAG	TCCCGGACGCGTCCACGTTCCGCCGCGGCGCCGCGCAGGGCCTGAGGGGGGCCCGGGCGTAGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCGCGGCGCCCAGGCACCAGCA	6393
	TGCTGGTGCCTGGGCGCCGCGCGCGCGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCTACGCCCGGGCCCCCCTCAGGCCCTGCGCGGCGCCGCGGCGGAACGTGGACGCGTCCGGGA	6394
	CCGGGCGTAGGCGGCGG	6395
	CCGCCGCCTACGCCCGG	6396
Waxy starch GBSS *Zea mays* Ser57Term CAG-TAG	GCGTCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCGCGGCGCCCAGGCACTAGCAGCAGGCGCGCCGCGGGGGCAGGTTCCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCA	6397
	TGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCCCCGCGGCGCGCCTGCTGCTAGTGCCTGGGCGCCGCGCGCGCGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGACGC	6398
	CCAGGCACTAGCAGCAG	6399
	CTGCTGCTAGTGCCTGG	6400

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Zea mays* Gln58Term CAG-TAG	TCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCG CGGCGCCCAGGCACCAGTAGCAGGCGCGCCGCGGGGGCAGGTT CCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCATGA	6401
	TCATGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCC CCGCGGCGCGCCTGCTACTGGTGCCTGGGCGCCGCGCGCGCGC TGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGA	6402
	GGCACCAGTAGCAGGCG	6403
	CGCCTGCTACTGGTGCC	6404

Example 11

<u>Altering fatty acid content of plants</u>

Improved means to manipulate fatty acid compositions, from biosynthetic or natural plant sources, are needed. For example, oils containing reduced saturated fatty acids are desired for dietary reasons and oils containing increased saturated fatty acids are also needed as alternatives to current sources of highly saturated oil products, such as tropical oils or chemically hydrogenated oils. It would therefore be advantageous to influence directly the production and composition of fatty acids in crop plants.

Higher plants synthesize fatty acids, primarily palmitic, stearic and oleic acids, in the plastids (i.e., chloroplasts, proplastids, or other related organelles) as part of the Fatty Acid Synthase (FAS) complex. Fatty acid synthesis is the result of the three enzymatic activities: acyl-ACP elongase, acyl-ACP desaturase and acyl-ACP thioesterases specific for each of palmitoyl-, stearoyl- and oleoyl-ACP.

A variety of enzymes have been identified that influence the relative levels of saturated vs. unsaturated fatty acids in plants. For example, the enzymes stearoyl-acyl carrier protein (stearoyl-ACP) desaturase, oleoyl desaturase and linoleate desaturase produce unsaturated fatty acids from saturated precursors. Similarly, relative enzymatic activities of the various acyl-ACP thioesterases influences the relative acyl-chain composition of the resultant fatty acids. Consequently a reduction or an increase of the activity of these enzymes can alter the properties of oils produced in a plant. In fact, specific targeting of particular enzymatic activities can results in altered levels of particular fatty acids.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes encoding proteins involved in fatty acid biosynthesis.

Table 22
Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Ser8Term TCG-TAG	TTTGGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGC CACCTCTGCTACGT<u>A</u>GTCATTCTTTCCTGTACCATCTTCTTCACTT GATCCTAATGGAAAAGGCAATAAGATTGG	6405
	CCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATGGTA CAGGAAAGAATGAC<u>T</u>ACGTAGCAGAGGTGGCCACCATGACGAGG AGATGAAGCGTTCAAAGACACTGCCACCAAA	6406

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCTACGT**A**GTCATTCT	6407
	AGAATGAC**T**ACGTAGCA	6408
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Ser9Term TCA-TGA	GGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGCCACCTCTGCTACGTCGT**G**ATTCTTTCCTGTACCATCTTCTTCACTTGATCCTAATGGAAAAGGCAATAAGATTGGGTC	6409
	GACCCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATGGTACAGGAAAGAAT**C**ACGACGTAGCAGAGGTGGCCACCATGACGAGGAGATGAAGCGTTCAAAGACACTGCCACC	6410
	TACGTCGT**G**ATTCTTTC	6411
	GAAAGAAT**C**ACGACGTA	6412
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Ser17Term TCA-TGA	ATCTCCTCGTCATGGTGGCCACCTCTGCTACGTCGTCATTCTTTCCTGTACCATCTTCTT**G**ACTTGATCCTAATGGAAAAGGCAATAAGATTGGGTCTACGAATCTTGCTGGACTCAATTC	6413
	GAATTGAGTCCAGCAAGATTCGTAGACCCAATCTTATTGCCTTTTCCATTAGGATCAAGT**C**AAGAAGATGGTACAGGAAAGAATGACGACGTAGCAGAGGTGGCCACCATGACGAGGAGAT	6414
	ATCTTCTT**G**ACTTGATC	6415
	GATCAAGT**C**AAGAAGAT	6416
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Gly22Term GGA-TGA	GTGGCCACCTCTGCTACGTCGTCATTCTTTCCTGTACCATCTTCTTCACTTGATCCTAAT**T**GAAAAGGCAATAAGATTGGGTCTACGAATCTTGCTGGACTCAATTCTGCACCTAACTCTG	6417
	CAGAGTTAGGTGCAGAATTGAGTCCAGCAAGATTCGTAGACCCAATCTTATTGCCTTTTC**A**ATTAGGATCAAGTGAAGAAGATGGTACAGGAAAGAATGACGACGTAGCAGAGGTGGCCAC	6418
	ATCCTAAT**T**GAAAAGGC	6419
	GCCTTTTC**A**ATTAGGAT	6420
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Ser8Term TCA-TGA	GCTTGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGT**G**ATCATTCTTTCCGTTGACTTCCCCTTCTGGGGATGCCAAATCGGGCAATCCCGGAAAAGG	6421
	CCTTTTCCGGGATTGCCCGATTTGGCATCCCCAGAAGGGGAAGTCAACGGAAAGAATGAT**C**ACGTGGCGGCAGTAGCAACCATTGTGGCCACAATTAACCAATCAGATCACAAATTCAAGC	6422
	CGCCACGT**G**ATCATTCT	6423
	AGAATGAT**C**ACGTGGCG	6424

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Ser9Term TCA-TGA	TGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGCTAC TGCCGCCACGTCAT**G**ATTCTTTCCGTTGACTTCCCCTTCTGGGGAT GCCAAATCGGGCAATCCCGGAAAAGGGTC	6425
	GACCCTTTTCCGGGATTGCCCGATTTGGCATCCCCAGAAGGGGAA GTCAACGGAAAGAAT**C**ATGACGTGGCGGCAGTAGCAACCATTGTG GCCACAATTAACCAATCAGATCACAAATTCA	6426
	CACGTCAT**G**ATTCTTTC	6427
	GAAAGAAT**C**ATGACGTG	6428
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Leu13Term TTG-TAG	CTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGT CATCATTCTTTCCGT**A**GACTTCCCCTTCTGGGGATGCCAAATCGG GCAATCCCGGAAAAGGGTCGGTGAGTTTTGG	6429
	CCAAAACTCACCGACCCTTTTCCGGGATTGCCCGATTTGGCATCC CCAGAAGGGGAAGTC**T**ACGGAAAGAATGATGACGTGGCGGCAGT AGCAACCATTGTGGCCACAATTAACCAATCAG	6430
	CTTTCCGT**A**GACTTCCC	6431
	GGGAAGTC**T**ACGGAAAG	6432
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Lys21Term AAA-TAA	ATGGTTGCTACTGCCGCCACGTCATCATTCTTTCCGTTGACTTCCC CTTCTGGGGATGCC**T**AATCGGGCAATCCCGGAAAAGGGTCGGTG AGTTTTGGGTCAATGAAGTCGAAATCCGCGG	6433
	CCGCGGATTTCGACTTCATTGACCCAAAACTCACCGACCCTTTTCC GGGATTGCCCGATT**A**GGCATCCCCAGAAGGGGAAGTCAACGGAA AGAATGATGACGTGGCGGCAGTAGCAACCAT	6434
	GGGATGCC**T**AATCGGGC	6435
	GCCCGATT**A**GGCATCCC	6436
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Ser8Term TCG-TAG	GGGATTTCAGCACGAAATTGAAGTTGTTTTTAAAAACCATGGTTGC TACTGCTGTGACAT**A**GGCGTTTTTCCCAGTCACTTCTTCACCTGAC TCCTCTGACTCGAAAAACAAGAAGCTCGG	6437
	CCGAGCTTCTTGTTTTTCGAGTCAGAGGAGTCAGGTGAAGAAGTG ACTGGGAAAAACGCC**T**ATGTCACAGCAGTAGCAACCATGGTTTTTA AAAACAACTTCAATTTCGTGCTGAAATCCC	6438
	TGTGACAT**A**GGCGTTTT	6439
	AAAACGCC**T**ATGTCACA	6440
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Ser16Term TCA-TGA	TGTTTTTAAAAACCATGGTTGCTACTGCTGTGACATCGGCGTTTTT CCCAGTCACTTCTT**G**ACCTGACTCCTCTGACTCGAAAAACAAGAAG CTCGGAAGCATCAAGTCGAAGCCATCGGT	6441
	ACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTTTTCGAGT CAGAGGAGTCAGGT**C**AAGAAGTGACTGGGAAAAACGCCGATGTCA CAGCAGTAGCAACCATGGTTTTTAAAAACA	6442

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CACTTCTTGACCTGACT	6443
	AGTCAGGTCAAGAAGTG	6444
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Ser22Term TCG-TAG	TTGCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACCTGACTCCTCTGACTAGAAAAACAAGAAGCTCGGAAGCATCAAGTCGAAGCCATCGGTTTCTTCTGGAAGTTTGCA	6445
	TGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTTTTCTAGTCAGAGGAGTCAGGTGAAGAAGTGACTGGGAAAAACGCCGATGTCACAGCAGTAGCAA	6446
	CTCTGACTAGAAAAACA	6447
	TGTTTTTCTAGTCAGAG	6448
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Lys23Term AAA-TAA	GCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACCTGACTCCTCTGACTCGTAAAACAAGAAGCTCGGAAGCATCAAGTCGAAGCCATCGGTTTCTTCTGGAAGTTTGCAAG	6449
	CTTGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTTTACGAGTCAGAGGAGTCAGGTGAAGAAGTGACTGGGAAAAACGCCGATGTCACAGCAGTAGC	6450
	CTGACTCGTAAAACAAG	6451
	CTTGTTTTACGAGTCAG	6452
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Ser14Term TCG-TAG	CTCCCGCTCGTTGAAAGACAATGGTGGCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTAGTCCCCGGTCACCTCCTCTAGACCAGGAAAGCCCGGAAATGGGTCATCGAGCTTCAGCCC	6453
	GGGCTGAAGCTCGATGACCCATTTCCGGGCTTTCCTGGTCTAGAGGAGGTGACCGGGGACTACACGGGGAAGAATGCAGAGCTTGCAGCGGTAGCCACCATTGTCTTTCAACGAGCGGGAG	6454
	CCCCGTGTAGTCCCCGG	6455
	CCGGGGACTACACGGGG	6456
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Arg21Term AGA-TGA	ATGGTGGCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACCTCCTCTTGACCAGGAAAGCCCGGAAATGGGTCATCGAGCTTCAGCCCCATCAAGCCCAAATTTGTCG	6457
	CGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTTCCGGGCTTTCCTGGTCAAGAGGAGGTGACCGGGGACGACACGGGGAAGAATGCAGAGCTTGCAGCGGTAGCCACCAT	6458
	CCTCCTCTTGACCAGGA	6459
	TCCTGGTCAAGAGGAGG	6460

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Gly23Term GGA-TGA	GCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACCTCCTCTAGACCATGAAAGCCCGGAAATGGGTCATCGAGCTTCAGCCCCATCAAGCCCAAATTTGTCGCCAATG	6461
	CATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTTCCGGGCTTTCATGGTCTAGAGGAGGTGACCGGGGACGACACGGGGAAGAATGCAGAGCTTGCAGCGGTAGC	6462
	CTAGACCATGAAAGCCC	6463
	GGGCTTTCATGGTCTAG	6464
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys24Term AAG-TAG	ACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACCTCCTCTAGACCAGGATAGCCCGGAAATGGGTCATCGAGCTTCAGCCCCATCAAGCCCAAATTTGTCGCCAATGGCG	6465
	CGCCATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTTCCGGGCTATCCTGGTCTAGAGGAGGTGACCGGGGACGACACGGGGAAGAATGCAGAGCTTGCAGCGGT	6466
	GACCAGGATAGCCCGGA	6467
	TCCGGGCTATCCTGGTC	6468
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Gly23Term GGA-TGA	GCCACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGTGAAAGCTCGGAAATGGGTCATCGAGCTTGAGCCCCCTCAAGCCCAAATTTGTCGCCAATG	6469
	CATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACCCATTTCCGAGCTTTCACGGCCTAGAGGAGGTGTCCGGGGACGGCAGGGGGAAGAATGCAGAACTTGCAGCGGTGGC	6470
	CTAGGCCGTGAAAGCTC	6471
	GAGCTTTCACGGCCTAG	6472
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Lys24Term AAG-TAG	ACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGGATAGCTCGGAAATGGGTCATCGAGCTTGAGCCCCCTCAAGCCCAAATTTGTCGCCAATGCCG	6473
	CGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACCCATTTCCGAGCTATCCCGGCCTAGAGGAGGTGTCCGGGGACGGCAGGGGGAAGAATGCAGAACTTGCAGCGGT	6474
	GGCCGGGATAGCTCGGA	6475
	TCCGAGCTATCCCGGCC	6476
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Gly26Term GGA-TGA	GCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGGAAAGCTCTGAAATGGGTCATCGAGCTTGAGCCCCCTCAAGCCCAAATTTGTCGCCAATGCCGGGTTGA	6477
	TCAACCCGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACCCATTTCAGAGCTTTCCCGGCCTAGAGGAGGTGTCCGGGGACGGCAGGGGGAAGAATGCAGAACTTGC	6478

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAAAGCTCTGAAATGGG	6479
	CCCATTTCAGAGCTTTC	6480
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Ser29Term TCA-TGA	CATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGGAA AGCTCGGAAATGGGTGATCGAGCTTGAGCCCCCTCAAGCCCAAAT TTGTCGCCAATGCCGGGTTGAAGGTTAAGGC	6481
	GCCTTAACCTTCAACCCGGCATTGGCGACAAATTTGGGCTTGAGG GGGCTCAAGCTCGATCACCCATTTCCGAGCTTTCCCGGCCTAGAG GAGGTGTCCGGGGACGGCAGGGGGAAGAATG	6482
	AAATGGGTGATCGAGCT	6483
	AGCTCGATCACCCATTT	6484
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Ser9Term TCG-TAG	CGTTTAAGTGGATCGGACATTTAAGTGTTTTAATCATGGTAGCTAT GAGTGCTACTGCGTAGCTGTTTCCGGTTTCTTCCCCAAAACCTCA CTCTGGAGCCAAGACATCTGATAAGCTTGG	6485
	CCAAGCTTATCAGATGTCTTGGCTCCAGAGTGAGGTTTTGGGGAA GAAACCGGAAACAGCTACGCAGTAGCACTCATAGCTACCATGATT AAAACACTTAAATGTCCGATCCACTTAAACG	6486
	TACTGCGTAGCTGTTTC	6487
	GAAACAGCTACGCAGTA	6488
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Lys17Term AAA-TAA	AGTGTTTTAATCATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTC CGGTTTCTTCCCCATAACCTCACTCTGGAGCCAAGACATCTGATAA GCTTGGAGGTGAACCAGGTAGTGTTGCTG	6489
	CAGCAACACTACCTGGTTCACCTCCAAGCTTATCAGATGTCTTGGC TCCAGAGTGAGGTTATGGGGAAGAAACCGGAAACAGCGACGCAG TAGCACTCATAGCTACCATGATTAAAACACT	6490
	CTTCCCCATAACCTCAC	6491
	GTGAGGTTATGGGGAAG	6492
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Gly21Term GGA-TGA	ATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCC CAAAACCTCACTCTTGAGCCAAGACATCTGATAAGCTTGGAGGTGA ACCAGGTAGTGTTGCTGTGCGCGGAATCA	6493
	TGATTCCGCGCACAGCAACACTACCTGGTTCACCTCCAAGCTTATC AGATGTCTTGGCTCAAGAGTGAGGTTTTGGGGAAGAAACCGGAAA CAGCGACGCAGTAGCACTCATAGCTACCAT	6494
	CTCACTCTTGAGCCAAG	6495
	CTTGGCTCAAGAGTGAG	6496

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Lys23Term AAG-TAG	GCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCCCAAAACCTCACTCTGGAGCC**T**AGACATCTGATAAGCTTGGAGGTGAACCAGGTAGTGTTGCTGTGCGCGGAATCAAGACAA	6497
	TTGTCTTGATTCCGCGCACAGCAACACTACCTGGTTCACCTCCAAGCTTATCAGATGTCT**A**GGCTCCAGAGTGAGGTTTTGGGGAAGAAACCGGAAACAGCGACGCAGTAGCACTCATAGC	6498
	CTGGAGCC**T**AGACATCT	6499
	AGATGTCT**A**GGCTCCAG	6500
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Lys21Term AAA-TAA	ATGGTGGCTGCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCT**T**AACCTGGGAAGTTAGGCAACTGGTCATCGAGTTTGAGCCCTTCCTTGAAGCCCAAGTCAA	6501
	TTGACTTGGGCTTCAAGGAAGGGCTCAAACTCGATGACCAGTTGCCTAACTTCCCAGGTT**A**AGGGGAGGCTCCTGGGGATGGAACAGGGAAGCATGCAGAACTTGCTGCAGCAGCCACCAT	6502
	CCTCCCCT**T**AACCTGGG	6503
	CCCAGGTT**A**AGGGGAGG	6504
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Lys24Term AAG-TAG	GCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGGG**T**AGTTAGGCAACTGGTCATCGAGTTTGAGCCCTTCCTTGAAGCCCAAGTCAATCCCCAATG	6505
	CATTGGGGATTGACTTGGGCTTCAAGGAAGGGCTCAAACTCGATGACCAGTTGCCTAACT**A**CCCAGGTTTAGGGGAGGCTCCTGGGGATGGAACAGGGAAGCATGCAGAACTTGCTGCAGC	6506
	AACCTGGG**T**AGTTAGGC	6507
	GCCTAACT**A**CCCAGGTT	6508
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Trp28Term TGG-TGA	TGCATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGGGAAGTTAGGCAACTG**A**TCATCGAGTTTGAGCCCTTCCTTGAAGCCCAAGTCAATCCCCAATGGCGGATTTCAGGTT	6509
	AACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAAGGGCTCAAACTCGATGA**T**CAGTTGCCTAACTTCCCAGGTTTAGGGGAGGCTCCTGGGGATGGAACAGGGAAGCATGCA	6510
	GGCAACTG**A**TCATCGAG	6511
	CTCGATGA**T**CAGTTGCC	6512
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Ser29Term TCA-TGA	CATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGGGAAGTTAGGCAACTGGT**G**ATCGAGTTTGAGCCCTTCCTTGAAGCCCAAGTCAATCCCCAATGGCGGATTTCAGGTTAA	6513
	TTAACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAAGGGCTCAAACTCGAT**C**ACCAGTTGCCTAACTTCCCAGGTTTAGGGGAGGCTCCTGGGGATGGAACAGGGAAGCATG	6514

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAACTGGT**G**ATCGAGTT	6515
	AACTCGAT**C**ACCAGTTG	6516
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys21Term AAA-TAA	ATGGTGGCTGCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACCCCGGGAATCTCCCCT**T**AACCCGGGAAGTTCGGTAATGGTGGCTTTCAGGTTAAGGCAAACGCCAATGCCCATCCTA	6517
	TAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGCCACCATTACCGAACTTCCCGGGTT**A**AGGGGAGATTCCCGGGGTTGGAACGGAGAAGAATGCAGAACTTGCTGCGGCAGCCACCAT	6518
	TCTCCCCT**T**AACCCGGG	6519
	CCCGGGTT**A**AGGGGAGA	6520
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys24Term AAG-TAG	GCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACCCCGGGAATCTCCCCTAAACCCGGG**T**AGTTCGGTAATGGTGGCTTTCAGGTTAAGGCAAACGCCAATGCCCATCCTAGTCTAAAGT	6521
	ACTTTAGACTAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGCCACCATTACCGAACT**A**CCCGGGTTTAGGGGAGATTCCCGGGGTTGGAACGGAGAAGAATGCAGAACTTGCTGCGGC	6522
	AACCCGGG**T**AGTTCGGT	6523
	ACCGAACT**A**CCCGGGTT	6524
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Gln31Term CAG-TAG	TTCTCCGTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTCGGTAATGGTGGCTTT**T**AGGTTAAGGCAAACGCCAATGCCCATCCTAGTCTAAAGTCTGGCAGCCTCGAGACTGAAG	6525
	CTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGGCATTGGCGTTTGCCTTAACCT**A**AAAGCCACCATTACCGAACTTCCCGGGTTTAGGGGAGATTCCCGGGGTTGGAACGGAGAA	6526
	GTGGCTTT**T**AGGTTAAG	6527
	CTTAACCT**A**AAAGCCAC	6528
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys33Term AAG-TAG	GTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTCGGTAATGGTGGCTTTCAGGTT**T**AGGCAAACGCCAATGCCCATCCTAGTCTAAAGTCTGGCAGCCTCGAGACTGAAGATGACA	6529
	TGTCATCTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGGCATTGGCGTTTGCCT**A**AACCTGAAAGCCACCATTACCGAACTTCCCGGGTTTAGGGGAGATTCCCGGGGTTGGAAC	6530
	TTCAGGTT**T**AGGCAAAC	6531
	GTTTGCCT**A**AACCTGAA	6532

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Gln21Term CAA-TAA	ATGTTGAAGCTCTCGTGTAATGCGACTGATAAGTTACAGACCCTCTTCTCGCATTCTCATTAACCGGATCCGGCACACCGGAGAACCGTCTCCTCCGTGTCGTGCTCTCATCTGAGGAAAC	6533
	GTTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCTCCGGTGTGCCGGATCCGGTTAATGAGAATGCGAGAAGAGGGTCTGTAACTTATCAGTCGCATTACACGAGAGCTTCAACAT	6534
	ATTCTCATTAACCGGAT	6535
	ATCCGGTTAATGAGAAT	6536
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Arg28Term AGA-TGA	GCGACTGATAAGTTACAGACCCTCTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGTGAACCGTCTCCTCCGTGTCGTGCTCTCATCTGAGGAAACCGGTTCTCGATCCTTTGCGAG	6537
	CTCGCAAAGGATCGAGAACCGGTTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCACCGGTGTGCCGGATCCGGTTGATGAGAATGCGAGAAGAGGGTCTGTAACTTATCAGTCGC	6538
	CACACCGGTGAACCGTC	6539
	GACGGTTCACCGGTGTG	6540
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Ser24Term TCG-TAG	CCCTCTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAACCGTCTCCTCCGTGTAGTGCTCTCATCTGAGGAAACCGGTTCTCGATCCTTTGCGAGCGATCGTATCTGCTGATCA	6541
	TGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTCCTCAGATGAGAGCACTACACGGAGGAGACGGTTCTCCGGTGTGCCGGATCCGGTTGATGAGAATGCGAGAAGAGGG	6542
	CTCCGTGTAGTGCTCTC	6543
	GAGAGCACTACACGGAG	6544
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Cys25Term TGC-TGA	CTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAACCGTCTCCTCCGTGTCGTGATCTCATCTGAGGAAACCGGTTCTCGATCCTTTGCGAGCGATCGTATCTGCTGATCAAGGA	6545
	TCCTTGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTCCTCAGATGAGATCACGACACGGAGGAGACGGTTCTCCGGTGTGCCGGATCCGGTTGATGAGAATGCGAGAAG	6546
	GTGTCGTGATCTCATCT	6547
	AGATGAGATCACGACAC	6548
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Leu2Term TTG-TAG	ATTCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGGGCATCAAAAATGTAGAAGCTTTCGTGTAATGTGACTAACAACTTACACACCTTCTCCTTCTTCTCCGATTCCTC	6549
	GAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCACATTACACGAAAGCTTCTACATTTTTGATGCCCTTTTTTTTTTATGGTTCCTGAGGTTTTGGTTTATAGAAGAAGAAT	6550

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAATGTAGAAGCTTT	6551
	AAAGCTTCTACATTTTT	6552
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Lys3Term AAG-TAG	TCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGGG CATCAAAAATGTTGTAGCTTTCGTGTAATGTGACTAACAACTTACAC ACCTTCTCCTTCTTCTCCGATTCCTCCC	6553
	GGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCA CATTACACGAAAGCTACAACATTTTTGATGCCCTTTTTTTTTTATGG TTCCTGAGGTTTTGGTTTATAGAAGAAGA	6554
	AAATGTTGTAGCTTTCG	6555
	CGAAAGCTACAACATTT	6556
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Ser5Term TCG-TAG	CTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGGGCATCAAA AATGTTGAAGCTTTAGTGTAATGTGACTAACAACTTACACACCTTCT CCTTCTTCTCCGATTCCTCCCTTTTCAT	6557
	ATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTG TTAGTCACATTACACTAAAGCTTCAACATTTTTGATGCCCTTTTTTTT TTATGGTTCCTGAGGTTTTGGTTTATAG	6558
	GAAGCTTTAGTGTAATG	6559
	CATTACACTAAAGCTTC	6560
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Cys6Term TGT-TGA	AAACCAAAACCTCAGGAACCATAAAAAAAAAAGGGCATCAAAAATG TTGAAGCTTTCGTGAAATGTGACTAACAACTTACACACCTTCTCCTT CTTCTCCGATTCCTCCCTTTTCATCCCG	6561
	CGGGATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTA AGTTGTTAGTCACATTTCACGAAAGCTTCAACATTTTTGATGCCCTT TTTTTTTTATGGTTCCTGAGGTTTTGGTTT	6562
	CTTTCGTGAAATGTGAC	6563
	GTCACATTTCACGAAAG	6564

Table 23
Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Lys4Term AAG-TAG	GGGAGAGCTCTAGCTCTGTAGAAAAGAAGGATTCATTCATCATATCCAGAAATGGCTCTATAGTTTAACCCTTTGGTGGCATCTCAGCCTTACAAATTCCCTTCCTCGACTCGTCCGCCAA	6565
	TTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCTGAGATGCCACCAAAGGGTTAAACTATAGAGCCATTTCTGGATATGATGAATGAATCCTTCTTTTCTACAGAGCTAGAGCTCTCCC	6566
	TGGCTCTATAGTTTAAC	6567
	GTTAAACTATAGAGCCA	6568
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Leu8Term TTG-TAG	CTCTGTAGAAAAGAAGGATTCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACCCTTAGGTGGCATCTCAGCCTTACAAATTCCCTTCCTCGACTCGTCCGCCAACTCCTTCTTTCAG	6569
	CTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCTGAGATGCCACCTAAGGGTTAAACTTTAGAGCCATTTCTGGATATGATGAATGAATCCTTCTTTTCTACAGAG	6570
	TAACCCTTAGGTGGCAT	6571
	ATGCCACCTAAGGGTTA	6572
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Gln12Term CAG-TAG	AGAAGGATTCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACCCTTTGGTGGCATCTTAGCCTTACAAATTCCCTTCCTCGACTCGTCCGCCAACTCCTTCTTTCAGATCTCCCAAGT	6573
	ACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCTAAGATGCCACCAAAGGGTTAAACTTTAGAGCCATTTCTGGATATGATGAATGAATCCTTCT	6574
	TGGCATCTTAGCCTTAC	6575
	GTAAGGCTAAGATGCCA	6576
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Phe14Term TAC-TAG	TCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACCCTTTGGTGGCATCTCAGCCTTAGAAATTCCCTTCCTCGACTCGTCCGCCAACTCCTTCTTTCAGATCTCCCAAGTTCCTCTGC	6577
	GCAGAGGAACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTTCTAAGGCTGAGATGCCACCAAAGGGTTAAACTTTAGAGCCATTTCTGGATATGATGAATGA	6578
	CAGCCTTAGAAATTCCC	6579
	GGGAATTTCTAAGGCTG	6580

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Brassica napus* Leu3Term TTG-TAG	GAGAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCAT**A**GAAGCTTAACCCTTTGGCATCTCAGCCTTACAAACTCCCTTCCTCGGCTCGTCCGCCAAT	6581
	ATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCTGAGATGCCAAAGGGTTAAGCTTC**T**ATGCCATTTTCTTTTTTTTGATACGAGGTTTGATGTTCTTTCAGACACGAGCGAGCTCTC	6582
	AATGGCAT**A**GAAGCTTA	6583
	TAAGCTTC**T**ATGCCATT	6584
Increased stearate stearoyl-ACP desaturase *Brassica napus* Lys4Term AAG-TAG	GAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATTG**T**AGCTTAACCCTTTGGCATCTCAGCCTTACAAACTCCCTTCCTCGGCTCGTCCGCCAATCT	6585
	AGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCTGAGATGCCAAAGGGTTAAGCT**A**CAATGCCATTTTCTTTTTTTTGATACGAGGTTTGATGTTCTTTCAGACACGAGCGAGCTC	6586
	TGGCATTG**T**AGCTTAAC	6587
	GTTAAGCT**A**CAATGCCA	6588
Increased stearate stearoyl-ACP desaturase *Brassica napus* Leu8Term TTG-TAG	TCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATTGAAGCTTAACCCTT**A**GGCATCTCAGCCTTACAAACTCCCTTCCTCGGCTCGTCCGCCAATCTCTACTCTCAGATC	6589
	GATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCTGAGATGCC**T**AAGGGTTAAGCTTCAATGCCATTTTCTTTTTTTTGATACGAGGTTTGATGTTCTTTCAGA	6590
	TAACCCTT**A**GGCATCTC	6591
	GAGATGCC**T**AAGGGTTA	6592
Increased stearate stearoyl-ACP desaturase *Brassica napus* Gln11Term CAG-TAG	AACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATTGAAGCTTAACCCTTTGGCATCT**T**AGCCTTACAAACTCCCTTCCTCGGCTCGTCCGCCAATCTCTACTCTCAGATCTCCCAAGT	6593
	ACTTGGGAGATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCT**A**AGATGCCAAAGGGTTAAGCTTCAATGCCATTTTCTTTTTTTTGATACGAGGTTTGATGTT	6594
	TGGCATCT**T**AGCCTTAC	6595
	GTAAGGCT**A**AGATGCCA	6596
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Gln27Term CAA-TAA	AACCAAAAGAAAAAGGTAAGAAAAAAAAACAATGGCTCTCAAGCTCAATCCTTTCCTTTCT**T**AAACCCAAAAGTTACCTTCTTTCGCTCTTCCACCAATGGCCAGTACCAGATCTCCTAAGT	6597
	ACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAGGTAACTTTTGGGTTT**A**AGAAAGGAAAGGATTGAGCTTGAGAGCCATTGTTTTTTTTTCTTACCTTTTTCTTTTGGTT	6598

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCTTTCTTAAACCCAA	6599
	TTGGGTTTAAGAAAGGA	6600
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Gln29Term CAA-TAA	AAGAAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTTTCCTTTCTCAAACCTAAAAGTTACCTTCTTTCGCTCTTCCACCAATGGCCAGTACCAGATCTCCTAAGTTCTACA	6601
	TGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAGGTAACTTTTAGGTTTGAGAAAGGAAAGGATTGAGCTTGAGAGCCATTGTTTTTTTTCTTACCTTTTTCTT	6602
	CTCAAACCTAAAAGTTA	6603
	TAACTTTTAGGTTTGAG	6604
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Lys30Term AAG-TAG	AAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTTTCCTTTCTCAAACCCAATAGTTACCTTCTTTCGCTCTTCCACCAATGGCCAGTACCAGATCTCCTAAGTTCTACATGG	6605
	CCATGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAGGTAACTATTGGGTTTGAGAAAGGAAAGGATTGAGCTTGAGAGCCATTGTTTTTTTTCTTACCTTTTT	6606
	AAACCCAATAGTTACCT	6607
	AGGTAACTATTGGGTTT	6608
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Lys46Term AAG-TAG	TCTCAAACCCAAAAGTTACCTTCTTTCGCTCTTCCACCAATGGCCAGTACCAGATCTCCTTAGTTCTACATGGCCTCTACCCTCAAGTCTGGTTCTAAGGAAGTTGAGAATCTCAAGAAGC	6609
	GCTTCTTGAGATTCTCAACTTCCTTAGAACCAGACTTGAGGGTAGAGGCCATGTAGAACTAAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAGGTAACTTTTGGGTTTGAGA	6610
	GATCTCCTTAGTTCTAC	6611
	GTAGAACTAAGGAGATC	6612
Increased stearate stearoyl-ACP desaturase *Glycine max* Gln11Term CAA-TAA	TCTTCTGATTCATTTAATCTTTACTCATCAATGGCTCTGAGACTGAACCCTATCCCCACCTAAACCTTCTCCCTCCCCCAAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTA	6613
	TAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTTGGGGGAGGGAGAAGGTTTAGGTGGGGATAGGGTTCAGTCTCAGAGCCATTGATGAGTAAAGATTAAATGAATCAGAAGA	6614
	TCCCCACCTAAACCTTC	6615
	GAAGGTTTAGGTGGGGA	6616

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Glycine max* Gln17Term CAA-TAA	CTTTACTCATCAATGGCTCTGAGACTGAACCCTATCCCCACCCAAACCTTCTCCCTCCCC**T**AAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTACCCTCCGCTCCGGTTCCA	6617
	TGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTT**A**GGGGAGGGAGAAGGTTTGGGTGGGGATAGGGTTCAGTCTCAGAGCCATTGATGAGTAAAG	6618
	CCCTCCCC**T**AAATGGCC	6619
	GGCCATTT**A**GGGGAGGG	6620
Increased stearate stearoyl-ACP desaturase *Glycine max* Arg22Term AGA-TGA	GCTCTGAGACTGAACCCTATCCCCACCCAAACCTTCTCCCTCCCCCAAATGGCCAGTCTC**T**GATCTCCCAGGTTCCGCATGGCCTCTACCCTCCGCTCCGGTTCCAAAGAGGTTGAAAATA	6621
	TATTTTCAACCTCTTTGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGATC**A**GAGACTGGCCATTTGGGGGAGGGAGAAGGTTTGGGTGGGGATAGGGTTCAGTCTCAGAGC	6622
	CCAGTCTC**T**GATCTCCC	6623
	GGGAGATC**A**GAGACTGG	6624
Increased stearate stearoyl-ACP desaturase *Glycine max* Lys37Term AAA-TAA	CAAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTACCCTCCGCTCCGGTTCC**T**AAGAGGTTGAAAATATTAAGAAGCCATTCACTCCTCCCAGAGAAGTGCATGTTCAAGTAA	6625
	TTACTTGAACATGCACTTCTCTGGGAGGAGTGAATGGCTTCTTAATATTTTCAACCTCTT**A**GGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTTG	6626
	CCGGTTCC**T**AAGAGGTT	6627
	AACCTCTT**A**GGAACCGG	6628
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Gln11Term CAA-TAA	CAACAAGCACACACAAGAACAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTT**T**AATCAGACCTGTACCGTTCATTCGCGTTTCCTCAACCGAAACCTCTCAGATCTCCCAAAT	6629
	ATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATGAACGGTACAGGTCTGATT**A**AAACGTCGCCGTATTGATGCGAATCGCCATTGTTGATGTTGTTCTTGTGTGTGCTTGTTG	6630
	CGACGTTT**T**AATCAGAC	6631
	GTCTGATT**A**AAACGTCG	6632
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Ser12Term TCA-TGA	AAGCACACACAAGAACAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTTCAAT**G**AGACCTGTACCGTTCATTCGCGTTTCCTCAACCGAAACCTCTCAGATCTCCCAAATTCGC	6633
	GCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATGAACGGTACAGGTCT**C**ATTGAAACGTCGCCGTATTGATGCGAATCGCCATTGTTGATGTTGTTCTTGTGTGTGCTT	6634

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTTCAATGAGACCTGT	6635
	ACAGGTCTCATTGAAAC	6636
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Tyr15Term TAC-TAG	AAGAACAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTTCAATCAGACCTGTAGCGTTCATTCGCGTTTCCTCAACCGAAACCTCTCAGATCTCCCAAATTCGCCATGGCTTCC	6637
	GGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATGAACGCTACAGGTCTGATTGAAACGTCGCCGTATTGATGCGAATCGCCATTGTTGATGTTGTTCTT	6638
	GACCTGTAGCGTTCATT	6639
	AATGAACGCTACAGGTC	6640
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Ser17Term TCA-TGA	CAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTTCAATCAGACCTGTACCGTTGATTCGCGTTTCCTCAACCGAAACCTCTCAGATCTCCCAAATTCGCCATGGCTTCCACCAT	6641
	ATGGTGGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATCAACGGTACAGGTCTGATTGAAACGTCGCCGTATTGATGCGAATCGCCATTGTTGATGTTG	6642
	GTACCGTTGATTCGCGT	6643
	ACGCGAATCAACGGTAC	6644
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Arg4Term CGA-TGA	ACACACAACACACACTCAATCACACACACATCATCATCTTCTTCATCAACGATGGCGCTTTGAATGAGTCCGGTGACGCTTCAACGGGAGATATATCCTTCATACACTTTTCATCAATCGA	6645
	TCGATTGATGAAAAGTGTATGAAGGATATATCTCCCGTTGAAGCGTCACCGGACTCATTCAAAGCGCCATCGTTGATGAAGAAGATGATGATGTGTGTGTGATTGAGTGTGTGTTGTGTGT	6646
	TGGCGCTTTGAATGAGT	6647
	ACTCATTCAAAGCGCCA	6648
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Gln11Term CAA-TAA	ACACACACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTGACGCTTTAACGGGAGATATATCCTTCATACACTTTTCATCAATCGAAAAATCTCAGATCTCCTAAAT	6649
	ATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGGATATATCTCCCGTTAAAGCGTCACCGGACTCATTCGAAGCGCCATCGTTGATGAAGAAGATGATGATGTGTGTGT	6650
	TGACGCTTTAACGGGAG	6651
	CTCCCGTTAAAGCGTCA	6652

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Glu13Term GAG-TAG	ACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTGACGCTTCAACGGTAGATATATCCTTCATACACTTTTCATCAATCGAAAAATCTCAGATCTCCTAAATTCGCGA	6653
	TCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGGATATATCTACCGTTGAAGCGTCACCGGACTCATTCGAAGCGCCATCGTTGATGAAGAAGATGATGATGT	6654
	TTCAACGGTAGATATAT	6655
	ATATATCTACCGTTGAA	6656
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Tyr15Term TAT-TAG	ATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTGACGCTTCAACGGGAGATATAGCCTTCATACACTTTTCATCAATCGAAAAATCTCAGATCTCCTAAATTCGCGATGGCTTCC	6657
	GGAAGCCATCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGGCTATATCTCCCGTTGAAGCGTCACCGGACTCATTCGAAGCGCCATCGTTGATGAAGAAGAT	6658
	GAGATATAGCCTTCATA	6659
	TATGAAGGCTATATCTC	6660
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Lys4Term AAG-TAG	AACTCAGCCAGCTTGCCCCCAAACAACAGCGCAGAAAAACCTTCAACAACAATGGCTCTCTAGCTCAACCCAGTCACCACCTTCCCTTCAACACGCTCCCTCAACAACTTCTCCTCCAGAT	6661
	ATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTTGAAGGGAAGGTGGTGACTGGGTTGAGCTAGAGAGCCATTGTTGTTGAAGGTTTTTCTGCGCTGTTGTTTGGGGGCAAGCTGGCTGAGTT	6662
	TGGCTCTCTAGCTCAAC	6663
	GTTGAGCTAGAGAGCCA	6664
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Ser13Term TCA-TGA	GCGCAGAAAAACCTTCAACAACAATGGCTCTCAAGCTCAACCCAGTCACCACCTTCCCTTGAACACGCTCCCTCAACAACTTCTCCTCCAGATCTCCTCGCACCTTTCTCATGGCTGCTTC	6665
	GAAGCAGCCATGAGAAAGGTGCGAGGAGATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTTCAAGGGAAGGTGGTGACTGGGTTGAGCTTGAGAGCCATTGTTGTTGAAGGTTTTTCTGCGC	6666
	CTTCCCTTGAACACGCT	6667
	AGCGTGTTCAAGGGAAG	6668
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Arg23Term AGA-TGA	CTCAAGCTCAACCCAGTCACCACCTTCCCTTCAACACGCTCCCTCAACAACTTCTCCTCCTGATCTCCTCGCACCTTTCTCATGGCTGCTTCCACTTTCAATTCCACCTCCACCAAGTAAG	6669
	CTTACTTGGTGGAGGTGGAATTGAAAGTGGAAGCAGCCATGAGAAAGGTGCGAGGAGATCAGGAGGAGAAGTTGTTGAGGGAGCGTGTTGAAGGGAAGGTGGTGACTGGGTTGAGCTTGAG	6670

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCTCCTCC**T**GATCTCCT	6671
	AGGAGATC**A**GGAGGAGA	6672
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Lys41Term AAG-TAG	TCCTCCAGATCTCCTCGCACCTTTCTCATGGCTGCTTCCACTTTCA ATTCCACCTCCACC**T**AGTAAGCATCTCCTCCTCCTCGGAATCTCCG CCGATTTCTTTTAAGCGATTGATCGTAGA	6673
	TCTACGATCAATCGCTTAAAAGAAATCGGCGGAGATTCCGAGGAG GAGGAGATGCTTACT**A**GGTGGAGGTGGAATTGAAAGTGGAAGCAG CCATGAGAAAGGTGCGAGGAGATCTGGAGGA	6674
	CCTCCACC**T**AGTAAGCA	6675
	TGCTTACT**A**GGTGGAGG	6676
Increased stearate stearoyl-ACP desaturase *Olea europaea* Arg21Term AGA-TGA	ATGGCACTGAAACTTTGCTTTCCACCCCACAAGATGCCTTCCTTCC CCGATGCTCGTATC**T**GATCTCACAGGGTTTTCATGGCTTCAACTAT TCATTCTCCTTCTATGGAGGTCGGAAAAG	6677
	CTTTTCCGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAA AACCCTGTGAGATC**A**GATACGAGCATCGGGGAAGGAAGGCATCTT GTGGGGTGGAAAGCAAAGTTTCAGTGCCAT	6678
	CTCGTATC**T**GATCTCAC	6679
	GTGAGATC**A**GATACGAG	6680
Increased stearate stearoyl-ACP desaturase *Olea europaea* Ser29Term TCA-TGA	CCCACAAGATGCCTTCCTTCCCCGATGCTCGTATCAGATCTCACA GGGTTTTCATGGCTT**G**AACTATTCATTCTCCTTCTATGGAGGTCGG AAAAGTTAAAAAGCCTTTCACGCCTCCACG	6681
	CGTGGAGGCGTGAAAGGCTTTTTAACTTTTCCGACCTCCATAGAAG GAGAATGAATAGTT**C**AAGCCATGAAAACCCTGTGAGATCTGATACG AGCATCGGGGAAGGAAGGCATCTTGTGGG	6682
	CATGGCTT**G**AACTATTC	6683
	GAATAGTT**C**AAGCCATG	6684
Increased stearate stearoyl-ACP desaturase *Olea europaea* Glu37Term GAG-TAG	GATGCTCGTATCAGATCTCACAGGGTTTTCATGGCTTCAACTATTC ATTCTCCTTCTATG**T**AGGTCGGAAAAGTTAAAAAGCCTTTCACGCC TCCACGAGAGGTACATGTTCAAGTAACCC	6685
	GGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAGGCTTTTT AACTTTTCCGACCT**A**CATAGAAGGAGAATGAATAGTTGAAGCCATG AAAACCCTGTGAGATCTGATACGAGCATC	6686
	CTTCTATG**T**AGGTCGGA	6687
	TCCGACCT**A**CATAGAAG	6688

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Olea europaea* Gly39Term GGA-TGA	CGTATCAGATCTCACAGGGTTTTCATGGCTTCAACTATTCATTCTCCTTCTATGGAGGTCTGAAAAGTTAAAAAGCCTTTCACGCCTCCACGAGAGGTACATGTTCAAGTAACCCATTCCT	6689
	AGGAATGGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAGGCTTTTTAACTTTTCAGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAAAACCCTGTGAGATCTGATACG	6690
	TGGAGGTCTGAAAAGTT	6691
	AACTTTTCAGACCTCCA	6692
Increased stearate stearoyl-ACP desaturase *Persea americana* Lys4Term AAA-TAA	TTCTCGTTTTTGTCGTCCCCTCTGCTCTCTCTCTATCAGGCACGGAGAAATGGCACTGTAACTCAGTCCAGTCATGTTTCAATCTCAGAAGCTTCCATTTCTTGCCTCCTATCCGCCTT	6693
	AAGGCGGATAGGAGGCAAGAAATGGAAGCTTCTGAGATTGAAACATGACTGGACTGAGTTACAGTGCCATTTCTCCGTGCCTGATAGAGAGAGAGAGCAGAGGGGACGACAAAAACGAGAA	6694
	TGGCACTGTAACTCAGT	6695
	ACTGAGTTACAGTGCCA	6696
Increased stearate stearoyl-ACP desaturase *Persea americana* Gln11Term CAA-TAA	CTGCTCTCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTCATGTTTTAATCTCAGAAGCTTCCATTTCTTGCCTCCTATCCGCCTTCCAATCTCAGATCTCCGAGGG	6697
	CCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAATGGAAGCTTCTGAGATTAAAACATGACTGGACTGAGTTTCAGTGCCATTTCTCCGTGCCTGATAGAGAGAGAGAGCAG	6698
	TCATGTTTTAATCTCAG	6699
	CTGAGATTAAAACATGA	6700
Increased stearate stearoyl-ACP desaturase *Persea americana* Gln13Term CAG-TAG	TCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTCATGTTTCAATCTTAGAAGCTTCCATTTCTTGCCTCCTATCCGCCTTCCAATCTCAGATCTCCGAGGGTTTTCA	6701
	TGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAATGGAAGCTTCTAAGATTGAAACATGACTGGACTGAGTTTCAGTGCCATTTCTCCGTGCCTGATAGAGAGAGA	6702
	TTCAATCTTAGAAGCTT	6703
	AAGCTTCTAAGATTGAA	6704
Increased stearate stearoyl-ACP desaturase *Persea americana* Lys14Term AAG-TAG	CTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTCATGTTTCAATCTCAGTAGCTTCCATTTCTTGCCTCCTATCCGCCTTCCAATCTCAGATCTCCGAGGGTTTTCATGG	6705
	CCATGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAATGGAAGCTACTGAGATTGAAACATGACTGGACTGAGTTTCAGTGCCATTTCTCCGTGCCTGATAGAGAG	6706

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCTCAG**T**AGCTTCCA	6707
	TGGAAGCT**A**CTGAGATT	6708
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Tyr12Term TAC-TAG	CCCCGAGATCTCGCTGCCGCTGCTCATGGCGTTCGCGGCGTCCCACACCGCATCGCCGTA**G**TCCTGCGGCGGCGTGGCGCAGAGGAGGAGCAATGGGATGTCGAAGATGGTGGCCATGGCC	6709
	GGCCATGGCCACCATCTTCGACATCCCATTGCTCCTCCTCTGCGCCACGCCGCCGCAGGA**C**TACGGCGATGCGGTGTGGGACGCCGCGAACGCCATGAGCAGCGGCAGCGAGATCTCGGGG	6710
	TCGCCGTA**G**TCCTGCGG	6711
	CCGCAGGA**C**TACGGCGA	6712
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Gln19Term CAG-TAG	CTGCTCATGGCGTTCGCGGCGTCCCACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCG**T**AGAGGAGGAGCAATGGGATGTCGAAGATGGTGGCCATGGCCTCCACCATCAACAGGGTCA	6713
	TGACCCTGTTGATGGTGGAGGCCATGGCCACCATCTTCGACATCCCATTGCTCCTCCTCT**A**CGCCACGCCGCCGCAGGAGTACGGCGATGCGGTGTGGGACGCCGCGAACGCCATGAGCAG	6714
	GCGTGGCG**T**AGAGGAGG	6715
	CCTCCTCT**A**CGCCACGC	6716
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Ser26Term TCG-TAG	CCCACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCGCAGAGGAGGAGCAATGGGATGT**A**GAAGATGGTGGCCATGGCCTCCACCATCAACAGGGTCAAGACTGCTAAGAAGCCCTACAC	6717
	GTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGGCCATGGCCACCATCTTC**T**ACATCCCATTGCTCCTCCTCTGCGCCACGCCGCCGCAGGAGTACGGCGATGCGGTGTGGG	6718
	TGGGATGT**A**GAAGATGG	6719
	CCATCTTC**T**ACATCCCA	6720
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Lys27Term AAG-TAG	CACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCGCAGAGGAGGAGCAATGGGATGTCG**T**AGATGGTGGCCATGGCCTCCACCATCAACAGGGTCAAGACTGCTAAGAAGCCCTACACTC	6721
	GAGTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGGCCATGGCCACCATCT**A**CGACATCCCATTGCTCCTCCTCTGCGCCACGCCGCCGCAGGAGTACGGCGATGCGGTGTG	6722
	GGATGTCG**T**AGATGGTG	6723
	CACCATCT**A**CGACATCC	6724

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Leu3Term TTG-TAG	TTCTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGA GAGAAGCAATGGCGTAGAAGCTTCACCACACGGCCTTCAATCCTT CCATGGCGGTTACCTCTTCGGGACTTCCTCG	6725
	CGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAGGC CGTGTGGTGAAGCTTCTACGCCATTGCTTCTCTCTCCTAAGTGCTT CTGTTGGTAACCGCTCAACCTAGAGAGAGAA	6726
	AATGGCGTAGAAGCTTC	6727
	GAAGCTTCTACGCCATT	6728
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Lys4Term AAG-TAG	CTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGAGA GAAGCAATGGCGTTGTAGCTTCACCACACGGCCTTCAATCCTTCC ATGGCGGTTACCTCTTCGGGACTTCCTCGAT	6729
	ATCGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTACAACGCCATTGCTTCTCTCTCCTAAGTG CTTCTGTTGGTAACCGCTCAACCTAGAGAGAG	6730
	TGGCGTTGTAGCTTCAC	6731
	GTGAAGCTACAACGCCA	6732
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Ser19Term TCG-TAG	AAGCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCAT GGCGGTTACCTCTTAGGGACTTCCTCGATCGTATCACCTCAGATC TCACCGCGTTTTCATGGCTTCTTCTACAAT	6733
	ATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGATAC GATCGAGGAAGTCCCTAAGAGGTAACCGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTTCAACGCCATTGCTT	6734
	TACCTCTTAGGGACTTC	6735
	GAAGTCCCTAAGAGGTA	6736
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Gly20Term GGA-TGA	GCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCATG GCGGTTACCTCTTCGTGACTTCCTCGATCGTATCACCTCAGATCTC ACCGCGTTTTCATGGCTTCTTCTACAATTG	6737
	CAATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGAT ACGATCGAGGAAGTCACGAAGAGGTAACCGCCATGGAAGGATTGA AGGCCGTGTGGTGAAGCTTCAACGCCATTGC	6738
	CCTCTTCGTGACTTCCT	6739
	AGGAAGTCACGAAGAGG	6740
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Ser21Term TCA-TGA	TGGCTCTGAATCTCAACCCCGTTTCCACACCATTTCAGTGTCGTCG ATTGCCGTCTTTCTGACCTCGTCAAACGCCTTCTCGCAGATCTCCC AAATTCTTCATGGCTTCCACTCTCAGCAG	6741
	CTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATCTGCGAGAA GGCGTTTGACGAGGTCAGAAAGACGGCAATCGACGACACTGAAAT GGTGTGGAAACGGGGTTGAGATTCAGAGCCA	6742

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTCTTTCT**G**ACCTCGTC	6743
	GACGAGGT**C**AGAAAGAC	6744
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Gln24Term CAA-TAA	AATCTCAACCCCGTTTCCACACCATTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGT**T**AAACGCCTTCTCGCAGATCTCCCAAATTCTTCATGGCTTCCACTCTCAGCAGCTCTTCTC	6745
	GAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATCTGCGAGAAGGCGTTT**A**ACGAGGTGAGAAAGACGGCAATCGACGACACTGAAATGGTGTGGAAACGGGGTTGAGATT	6746
	CACCTCGT**T**AAACGCCT	6747
	AGGCGTTT**A**ACGAGGTG	6748
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Arg29Term AGA-TGA	TCCACACCATTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTCAAACGCCTTCTCGC**T**GATCTCCCAAATTCTTCATGGCTTCCACTCTCAGCAGCTCTTCTCCTAAGGAAGCGGAAA	6749
	TTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATC**A**GCGAGAAGGCGTTTGACGAGGTGAGAAAGACGGCAATCGACGACACTGAAATGGTGTGGA	6750
	CTTCTCGC**T**GATCTCCC	6751
	GGGAGATC**A**GCGAGAAG	6752
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Lys32Term AAA-TAA	TTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTCAAACGCCTTCTCGCAGATCTCCC**T**AATTCTTCATGGCTTCCACTCTCAGCAGCTCTTCTCCTAAGGAAGCGGAAAGCCTGAAGA	6753
	TCTTCAGGCTTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATT**A**GGGAGATCTGCGAGAAGGCGTTTGACGAGGTGAGAAAGACGGCAATCGACGACACTGAAA	6754
	GATCTCCC**T**AATTCTTC	6755
	GAAGAATT**A**GGGAGATC	6756
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Leu10Term TTA-TGA	AAATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCGT**G**AAAATCTCACAAAATGTTACCATTTCCTTGTTCTTCAGCCAGATCTGAGCGAGTTTTCAT	6757
	ATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAACATTTTGTGAGATTTT**C**ACGACACCCCATTGATATTCAGTGCCATTGTTGATGCTCTGTTTTTCACCTCGACTATTT	6758
	GGTGTCGT**G**AAAATCTC	6759
	GAGATTTT**C**ACGACACC	6760

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Lys11Term AAA-TAA	ATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCGTTA**T**AATCTCACAAAATGTTACCATTTCCTTGTTCTTCAGCCAGATCTGAGCGAGTTTTCATGG	6761
	CCATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAACATTTTGTGAGATT**A**TAACGACACCCCATTGATATTCAGTGCCATTGTTGATGCTCTGTTTTTCACCTCGACTAT	6762
	TGTCGTTA**T**AATCTCAC	6763
	GTGAGATT**A**TAACGACA	6764
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Lys14Term AAA-TAA	GTGAAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCGTTAAAATCTCAC**T**AAATGTTACCATTTCCTTGTTCTTCAGCCAGATCTGAGCGAGTTTTCATGGCTTCAACCA	6765
	TGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAACATTT**A**GTGAGATTTTAACGACACCCCATTGATATTCAGTGCCATTGTTGATGCTCTGTTTTTCAC	6766
	AATCTCAC**T**AAATGTTA	6767
	TAACATTT**A**GTGAGATT	6768
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Leu16Term TTA-TGA	ACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCGTTAAAATCTCACAAAATGT**G**ACCATTTCCTTGTTCTTCAGCCAGATCTGAGCGAGTTTTCATGGCTTCAACCATTCATCG	6769
	CGATGAATGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGT**C**ACATTTTGTGAGATTTTAACGACACCCCATTGATATTCAGTGCCATTGTTGATGCTCTGT	6770
	CAAAATGT**G**ACCATTTC	6771
	GAAATGGT**C**ACATTTTG	6772
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser21Term TCA-TGA	TGGCTCTGAGGCTGAACCCTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCAT**G**ATCTTCTTCTTCTTCATCGTTCTCGCTTCCTCAAATGGCTAGCCTCAGATCTCCAAGGTT	6773
	AACCTTGGAGATCTGAGGCTAGCCATTTGAGGAAGCGAGAACGATGAAGAAGAAGAAGAT**C**ATGATGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAGGGTTCAGCCTCAGAGCCA	6774
	TTCATCAT**G**ATCTTCTT	6775
	AAGAAGAT**C**ATGATGAA	6776
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser26Term TCA-TGA	ACCCTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCTTCTTCTTCTT**G**ATCGTTCTCGCTTCCTCAAATGGCTAGCCTCAGATCTCCAAGGTTCCGCATGGCCTCCAC	6777
	GTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCATTTGAGGAAGCGAGAACGAT**C**AAGAAGAAGAAGATGATGATGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAGGGT	6778

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTCTTCTTGATCGTTCT	6779
	AGAACGATCAAGAAGAA	6780
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser27Term TCG-TAG	CTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCT TCTTCTTCTTCATAGTTCTCGCTTCCTCAAATGGCTAGCCTCAGAT CTCCAAGGTTCCGCATGGCCTCCACCCT	6781
	AGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCAT TTGAGGAAGCGAGAACTATGAAGAAGAAGAAGATGATGATGAAGA AGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAG	6782
	TTCTTCATAGTTCTCGC	6783
	GCGAGAACTATGAAGAA	6784
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser29Term TCG-TAG	CTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCTTCTTCT TCTTCATCGTTCTAGCTTCCTCAAATGGCTAGCCTCAGATCTCCAA GGTTCCGCATGGCCTCCACCCTCCGCAC	6785
	GTGCGGAGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCT AGCCATTTGAGGAAGCTAGAACGATGAAGAAGAAGAAGATGATGA TGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAG	6786
	ATCGTTCTAGCTTCCTC	6787
	GAGGAAGCTAGAACGAT	6788
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Leu3Term TTG-TAG	AAAGTTAAAAGCCGTCCAAAACCCAAACCAGGAAAGGCAAACGAA AAGAAAAAAATGGCTTAGAATTTTAATGCCATCGCCTCGAAATCTCA GAAGCTCCCTTGCTTTGCTCTTCCACCAAA	6789
	TTTGGTGGAAGAGCAAAGCAAGGGAGCTTCTGAGATTTCGAGGCG ATGGCATTAAAATTCTAAGCCATTTTTTTCTTTTCGTTTGCCTTTCCT GGTTTGGGTTTTGGACGGCTTTTAACTTT	6790
	AATGGCTTAGAATTTTA	6791
	TAAAATTCTAAGCCATT	6792
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Ser1-Term TCG-TAG	CCCAAACCAGGAAAGGCAAACGAAAAGAAAAAAATGGCTTTGAATTT TAATGCCATCGCCTAGAAATCTCAGAAGCTCCCTTGCTTTGCTCTT CCACCAAAGGCCACCCTTAGATCTCCCAA	6793
	TTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAAAGCAAGG GAGCTTCTGAGATTTCTAGGCGATGGCATTAAAATTCAAAGCCATT TTTTCTTTTCGTTTGCCTTTCCTGGTTTGGG	6794
	CATCGCCTAGAAATCTC	6795
	GAGATTTCTAGGCGATG	6796

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Lys11Term AAA-TAA	CAAACCAGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTTTAATGCCATCGCCTCGTAATCTCAGAAGCTCCCTTGCTTTGCTCTTCCACCAAAGGCCACCCTTAGATCTCCCAAGT	6797
	ACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAAAGCAAGGGAGCTTCTGAGATTACGAGGCGATGGCATTAAAATTCAAAGCCATTTTTTCTTTTCGTTTGCCTTTCCTGGTTTG	6798
	TCGCCTCGTAATCTCAG	6799
	CTGAGATTACGAGGCGA	6800
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Gln13Term CAG-TAG	AGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTTTAATGCCATCGCCTCGAAATCTTAGAAGCTCCCTTGCTTTGCTCTTCCACCAAAGGCCACCCTTAGATCTCCCAAGTTTTCCA	6801
	TGGAAAACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAAAGCAAGGGAGCTTCTAAGATTTCGAGGCGATGGCATTAAAATTCAAAGCCATTTTTTCTTTTCGTTTGCCTTTCCT	6802
	CGAAATCTTAGAAGCTC	6803
	GAGCTTCTAAGATTTCG	6804

Table 24
Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Ser4Term TCG-TAG	AATAGAACGACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGC TCCAATGGCGAGCTAGGTTTTATCAGAATGTGGTTTTAGACCTCTC CCCAGATTCTACCCTAAACACACAACCTC	6805
	GAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTAAAACCA CATTCTGATAAAACCTAGCTCGCCATTGGAGCCTCTTCCCAAGAAG AAAAGAGGAAAAAGTCTCTGTCGTTCTATT	6806
	GGCGAGCTTGGTTTTAT	6807
	ATAAAACCAAGCTCGCC	6808
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Leu6Term TTA-TGA	ACGACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAAT GGCGAGCTCGGTTTGATCAGAATGTGGTTTTAGACCTCTCCCCAG ATTCTACCCTAAACACACAACCTCTTTTGC	6809
	GCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTA AAACCACATTCTGATCAAACCGAGCTCGCCATTGGAGCCTCTTCC CAAGAAGAAAAGAGGAAAAAGTCTCTGTCGT	6810
	CTCGGTTTGATCAGAAT	6811
	ATTCTGATCAAACCGAG	6812
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Ser7Term TCA-TGA	ACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAATGGC GAGCTCGGTTTTATGAGAATGTGGTTTTAGACCTCTCCCCAGATTC TACCCTAAACACACAACCTCTTTTGCCTC	6813
	GAGGCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGT CTAAAACCACATTCTCATAAAACCGAGCTCGCCATTGGAGCCTCTT CCCAAGAAGAAAAGAGGAAAAAGTCTCTGT	6814
	GGTTTTATGAGAATGTG	6815
	CACATTCTCATAAAACC	6816
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Glu8Term GAA-TAA	AGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAATGGCGA GCTCGGTTTTATCATAATGTGGTTTTAGACCTCTCCCCAGATTCTA CCCTAAACACACAACCTCTTTTGCCTCTA	6817
	TAGAGGCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAG GTCTAAAACCACATTATGATAAAACCGAGCTCGCCATTGGAGCCTC TTCCCAAGAAGAAAAGAGGAAAAAGTCTCT	6818
	TTTTATCATAATGTGGT	6819
	ACCACATTATGATAAAA	6820

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Leu4Term TTG-TAG	TCATCATCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACTAGGTCTTATCCGAATGTGGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCAC	6821
	GTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCACATTCGGATAAGACCTAGTTCGCCATTGCTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAGAAGAAGAAGATGATGA	6822
	GGCGAACTAGGTCTTAT	6823
	ATAAGACCTAGTTCGCC	6824
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Leu6Term TTA-TGA	TCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACTTGGTCTGATCCGAATGTGGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCACTTTCCT	6825
	AGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCACATTCGGATCAGACCAAGTTCGCCATTGCTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAGAAGAAGAAGA	6826
	CTTGGTCTGATCCGAAT	6827
	ATTCGGATCAGACCAAG	6828
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Glu8Term GAA-TAA	TTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACTTGGTCTTATCCTAATGTGGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCACTTTCCTCTCCA	6829
	TGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCACATTAGGATAAGACCAAGTTCGCCATTGCTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAGAAGAA	6830
	TCTTATCCTAATGTGGC	6831
	GCCACATTAGGATAAGA	6832
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Cys9Term TGT-TGA	CTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACTTGGTCTTATCCGAATGAGGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCACTTTCCTCTCCAACACC	6833
	GGTGTTGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCTCATTCGGATAAGACCAAGTTCGCCATTGCTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAG	6834
	TCCGAATGAGGCATAAG	6835
	CTTATGCCTCATTCGGA	6836
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Trp5Term TGG-TGA	ATAACAGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTGGTTGAGTATTATCAGAATGTGGTTTAAGGCCTCTCCCAAGAATCTACTCACGACCCAGAATTGGT	6837
	ACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACCACATTCTGATAATACTCAACCAGCAGCCATTGAAAACCCAGAAGCTAAAAATGCAAGAATTCAGCAATTCTGTTAT	6838

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCTGGTTGAGTATTATC	6839
	GATAATACTCAACCAGC	6840
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Leu7Term TTA-TGA	AGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTGGTTGGGTATGATCAGAATGTGGTTTAAGGCCTCTCCCAAGAATCTACTCACGACCCAGAATTGGTTTTAC	6841
	GTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACCACATTCTGATCATACCCAACCAGCAGCCATTGAAAACCCAGAAGCTAAAAATGCAAGAATTCAGCAATTCT	6842
	TTGGGTATGATCAGAAT	6843
	ATTCTGATCATACCCAA	6844
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Ser8Term TCA-TGA	ATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTGGTTGGGTATTATGAGAATGTGGTTTAAGGCCTCTCCCAAGAATCTACTCACGACCCAGAATTGGTTTTACATC	6845
	GATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACCACATTCTCATAATACCCAACCAGCAGCCATTGAAAACCCAGAAGCTAAAAATGCAAGAATTCAGCAAT	6846
	GGTATTATGAGAATGTG	6847
	CACATTCTCATAATACC	6848
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Glu9Term GAA-TAA	TGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTGGTTGGGTATTATCATAATGTGGTTTAAGGCCTCTCCCAAGAATCTACTCACGACCCAGAATTGGTTTTACATCGA	6849
	TCGATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACCACATTATGATAATACCCAACCAGCAGCCATTGAAAACCCAGAAGCTAAAAATGCAAGAATTCAGCA	6850
	TATTATCATAATGTGGT	6851
	ACCACATTATGATAATA	6852
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Arg22Term AGA-TGA	GCAAGTTGGGTTTTATCAGAATGTGGTCTTAGACCACTCCCAAGAATCTACCCTAAGCCCTGAACTGGGGCAGCCACTTCTGCCTCCTCTCACATTAAGTTGAGAATTTCACGTACAGATC	6853
	GATCTGTACGTGAAATTCTCAACTTAATGTGAGAGGAGGCAGAAGTGGCTGCCCCAGTTCAGGGCTTAGGGTAGATTCTTGGGAGTGGTCTAAGACCACATTCTGATAAAACCCAACTTGC	6854
	CTAAGCCCTGAACTGGG	6855
	CCCAGTTCAGGGCTTAG	6856

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Lys34Term AAG-TAG	CTCCCAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCCTCTCACATTTAGTTGAGAATTTCACGTACAGATCTGAGTGGTTCTGCAATTTCTTTGTCTAATACTAATA	6857
	TATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACGTGAAATTCTCAACTAAATGTGAGAGGAGGCAGAAGTGGCTGCCCCAGTTCTGGGCTTAGGGTAGATTCTTGGGAG	6858
	CTCACATTTAGTTGAGA	6859
	TCTCAACTAAATGTGAG	6860
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Leu35Term TTG-TAG	CAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCCTCTCACATTAAGTAGAGAATTTCACGTACAGATCTGAGTGGTTCTGCAATTTCTTTGTCTAATACTAATAAAGA	6861
	TCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACGTGAAATTCTCTACTTAATGTGAGAGGAGGCAGAAGTGGCTGCCCCAGTTCTGGGCTTAGGGTAGATTCTTG	6862
	CATTAAGTAGAGAATTT	6863
	AAATTCTCTACTTAATG	6864
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Arg36Term AGA-TGA	AGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCCTCTCACATTAAGTTGTGAATTTCACGTACAGATCTGAGTGGTTCTGCAATTTCTTTGTCTAATACTAATAAAGAGA	6865
	TCTCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACGTGAAATTCACAACTTAATGTGAGAGGAGGCAGAAGTGGCTGCCCCAGTTCTGGGCTTAGGGTAGATTCT	6866
	TTAAGTTGTGAATTTCA	6867
	TGAAATTCACAACTTAA	6868
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Arg22Term AGA-TGA	GCGAGTTGGGTTTTATCAGAATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCATGAACTGGCCACCCTTTGTTGAATTCCAATCCCACAAAGCTGAGATTTTCAAGAACAGATC	6869
	GATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTCAACAAAGGGTGGCCAGTTCATGGCTTAGGATAGACCCTCGGGAGTGGCCTCAGACCACATTCTGATAAAACCCAACTCGC	6870
	CTAAGCCATGAACTGGC	6871
	GCCAGTTCATGGCTTAG	6872
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Leu27Term TTG-TAG	CAGAATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTAGTTGAATTCCAATCCCACAAAGCTGAGATTTTCAAGAACAGATCTTGGAAATGGTTCTTC	6873
	GAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTCAACTAAGGGTGGCCAGTTCTTGGCTTAGGATAGACCCTCGGGAGTGGCCTCAGACCACATTCTG	6874

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCACCCTTAGTTGAATT	6875
	AATTCAACTAAGGGTGG	6876
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Leu28Term TTG-TAG	AATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGTAGAATTCCAATCCCACAAAGCTGAGATTTTCAAGAACAGATCTTGGAAATGGTTCTTCATT	6877
	AATGAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTCTACAAAGGGTGGCCAGTTCTTGGCTTAGGATAGACCCTCGGGAGTGGCCTCAGACCACATT	6878
	CCCTTTGTAGAATTCCA	6879
	TGGAATTCTACAAAGGG	6880
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Lys34Term AAG-TAG	CTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGTTGAATTCCAATCCCACATAGCTGAGATTTTCAAGAACAGATCTTGGAAATGGTTCTTCATTCTGTTTGTCGAGTGGGA	6881
	TCCCACTCGACAAACAGAATGAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTATGTGGGATTGGAATTCAACAAAGGGTGGCCAGTTCTTGGCTTAGGATAGACCCTCGGGAG	6882
	ATCCCACATAGCTGAGA	6883
	TCTCAGCTATGTGGGAT	6884
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Tyr3Term TAC-TAG	CATCAGAGCGGCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCTATGAGTTAGGTCGTCAGAGAGCTAGCCATCGTGTTCGCACTAGCTGCTGGAGCTGCTTACCTCAACAAT	6885
	ATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGCTAGCTCTCTGACGACCTAACTCATAGACTTCCATGGATTCTTAACCCAGCAATGCTTAGGTATCGCCGCTCTGATG	6886
	ATGAGTTAGGTCGTCAG	6887
	CTGACGACCTAACTCAT	6888
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Arg6Term AGA-TGA	GCGGCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCTATGAGTTACGTCGTCTGAGAGCTAGCCATCGTGTTCGCACTAGCTGCTGGAGCTGCTTACCTCAACAATTGGCTTG	6889
	CAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGCTAGCTCTCAGACGACGTAACTCATAGACTTCCATGGATTCTTAACCCAGCAATGCTTAGGTATCGCCGC	6890
	ACGTCGTCTGAGAGCTA	6891
	TAGCTCTCAGACGACGT	6892

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Glu7Term GAG-TAG	GCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCTATGAGTTACGTCGTCAGATAGCTAGCCATCGTGTTCGCACTAGCTGCTGGAGCTGCTTACCTCAACAATTGGCTTGTTT	6893
	AAACAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGCTAGCTATCTGACGACGTAACTCATAGACTTCCATGGATTCTTAACCCAGCAATGCTTAGGTATCGC	6894
	TCGTCAGATAGCTAGCC	6895
	GGCTAGCTATCTGACGA	6896
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Gly17Term GGA-TGA	CCATGGAAGTCTATGAGTTACGTCGTCAGAGAGCTAGCCATCGTGTTCGCACTAGCTGCTTGAGCTGCTTACCTCAACAATTGGCTTGTTTGGCCTCTCTATTGGATTGCTCAAGGAACCA	6897
	TGGTTCCTTGAGCAATCCAATAGAGAGGCCAAACAAGCCAATTGTTGAGGTAAGCAGCTCAAGCAGCTAGTGCGAACACGATGGCTAGCTCTCTGACGACGTAACTCATAGACTTCCATGG	6898
	TAGCTGCTTGAGCTGCT	6899
	AGCAGCTCAAGCAGCTA	6900
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Arg22Term AGA-TGA	GCAAGTTGGGTTCTATCAGAATGTGGTCTTAGACCACTACCAAGAATATACCCAAAGCCCTGAATAGGGTCTTCTTCCGTTTGCGCCACCAATTTAAATCTGAGAAGAATTTCACCTTCAC	6901
	GTGAAGGTGAAATTCTTCTCAGATTTAAATTGGTGGCGCAAACGGAAGAAGACCCTATTCAGGGCTTTGGGTATATTCTTGGTAGTGGTCTAAGACCACATTCTGATAGAACCCAACTTGC	6902
	CAAAGCCCTGAATAGGG	6903
	CCCTATTCAGGGCTTTG	6904
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Cys29Term TGC-TGA	TGGTCTTAGACCACTACCAAGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTGAGCCACCAATTTAAATCTGAGAAGAATTTCACCTTCACCTATACGAACAGATCGGAATTGT	6905
	ACAATTCCGATCTGTTCGTATAGGTGAAGGTGAAATTCTTCTCAGATTTAAATTGGTGGCTCAAACGGAAGAAGACCCTATTCTGGGCTTTGGGTATATTCTTGGTAGTGGTCTAAGACCA	6906
	TCCGTTTGAGCCACCAA	6907
	TTGGTGGCTCAAACGGA	6908
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Leu33Term TTA-TGA	CACTACCAAGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTGCGCCACCAATTGAAATCTGAGAAGAATTTCACCTTCACCTATACGAACAGATCGGAATTGTTGGGCATTGAG	6909
	CTCAATGCCCAACAATTCCGATCTGTTCGTATAGGTGAAGGTGAAATTCTTCTCAGATTTCAATTGGTGGCGCAAACGGAAGAAGACCCTATTCTGGGCTTTGGGTATATTCTTGGTAGTG	6910

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CACCAATT**G**AAATCTGA	6911
	TCAGATTT**C**AATTGGTG	6912
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Arg36Term AGA-TGA	AGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTGCGCCA CCAATTTAAATCTG**T**GAAGAATTTCACCTTCACCTATACGAACAGAT CGGAATTGTTGGGCATTGAGGGTAAGTG	6913
	CACTTACCCTCAATGCCCAACAATTCCGATCTGTTCGTATAGGTGA AGGTGAAATTCTTC**A**CAGATTTAAATTGGTGGCGCAAACGGAAGAA GACCCTATTCTGGGCTTTGGGTATATTCT	6914
	TAAATCTG**T**GAAGAATT	6915
	AATTCTTC**A**CAGATTTA	6916
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Trp4Term TGG-TGA	CTCTTTATTATCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACC TATGGCAAGTTG**A**GTGATTTCAGAATGTGGGCTAAGGCCACTTCC AAGAATCTATGCCAGGCCCAGAAGTGGA	6917
	TCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGCCTTAGCCC ACATTCTGAAATCAC**T**CAACTTGCCATAGGTGACTCAGAACTCAAA AAAAACAAAGAAGAGGAGGATAATAAAGAG	6918
	GCAAGTTG**A**GTGATTTC	6919
	GAAATCAC**T**CAACTTGC	6920
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Ser7Term TCA-TGA	TATCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCA AGTTGGGTGATTT**G**AGAATGTGGGCTAAGGCCACTTCCAAGAATC TATGCCAGGCCCAGAAGTGGAGCTTCATG	6921
	CATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGC CTTAGCCCACATTCT**C**AAATCACCCAACTTGCCATAGGTGACTCAG AACTCAAAAAAAACAAAGAAGAGGAGGATA	6922
	GGTGATTT**G**AGAATGTG	6923
	CACATTCT**C**AAATCACC	6924
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Glu8Term GAA-TAA	TCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAG TTGGGTGATTTCA**T**AATGTGGGCTAAGGCCACTTCCAAGAATCTAT GCCAGGCCCAGAAGTGGAGCTTCATGTT	6925
	AACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTG GCCTTAGCCCACATT**A**TGAAATCACCCAACTTGCCATAGGTGACTC AGAACTCAAAAAAAACAAAGAAGAGGAGGA	6926
	TGATTTCA**T**AATGTGGG	6927
	CCCACATT**A**TGAAATCA	6928

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Cys9Term TGT-TGA	CTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAGTTGGGTGATTTCAGAATGAGGGCTAAGGCCACTTCCAAGAATCTATGCCAGGCCCAGAAGTGGAGCTTCATGTTTCAAC	6929
	GTTGAAACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGCCTTAGCCCTCATTCTGAAATCACCCAACTTGCCATAGGTGACTCAGAACTCAAAAAAAACAAAGAAGAG	6930
	TCAGAATGAGGGCTAAG	6931
	CTTAGCCCTCATTCTGA	6932
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Lys21Term AAA-TAA	ATGAAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTTTTCATGCTTAAGAAGAAGAAGAAGAAGAGGATTTCGACTTAAGCAATCCTCCTCCATTCAATATTGGTC	6933
	GACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTCTTCTTCTTCTTCTTAAGCATGAAAACCATTAACGCCATTTAGAATTGGGGTGTCTTTGTACTGTTGCTGCTTCAT	6934
	TTCATGCTTAAGAAGAA	6935
	TTCTTCTTAAGCATGAA	6936
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Glu22Term GAA-TAA	AAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTTTTCATGCTAAATAAGAAGAAGAAGAAGAGGATTTCGACTTAAGCAATCCTCCTCCATTCAATATTGGTCAGA	6937
	TCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTCTTCTTCTTCTTATTTAGCATGAAAACCATTAACGCCATTTAGAATTGGGGTGTCTTTGTACTGTTGCTGCTT	6938
	ATGCTAAATAAGAAGAA	6939
	TTCTTCTTATTTAGCAT	6940
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Glu23Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTTTTCATGCTAAAGAATAAGAAGAAGAAGAGGATTTCGACTTAAGCAATCCTCCTCCATTCAATATTGGTCAGATCC	6941
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTCTTCTTCTTATTCTTTAGCATGAAAACCATTAACGCCATTTAGAATTGGGGTGTCTTTGTACTGTTGCTG	6942
	CTAAAGAATAAGAAGAA	6943
	TTCTTCTTATTCTTTAG	6944
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Glu24Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTTTTCATGCTAAAGAATAAGAAGAAGAAGAGGATTTCGACTTAAGCAATCCTCCTCCATTCAATATTGGTCAGATCC	6945
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTCTTCTTCTTATTCTTTAGCATGAAAACCATTAACGCCATTTAGAATTGGGGTGTCTTTGTACTGTTGCTG	6946

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTAAAGAA**T**AAGAAGAA	6947
	TTCTTCTT**A**TTCTTTAG	6948
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Tyr21Term TAT-TAG	GGTCCAAGCACAGCCTCTACAACATGTTGGTAATGGTGCAGGGAAAGAAGATCAAGCTTA**G**TTTGATCCAAGTGCTCCACCACCCTTCAAGATTGCAAATATCAGAGCAGCAATTCCAAAA	6949
	TTTTGGAATTGCTGCTCTGATATTTGCAATCTTGAAGGGTGGTGGAGCACTTGGATCAAA**C**TAAGCTTGATCTTCTTTCCCTGCACCATTACCAACATGTTGTAGAGGCTGTGCTTGGACC	6950
	CAAGCTTA**G**TTTGATCC	6951
	GGATCAAA**C**TAAGCTTG	6952
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Lys31Term AAG-TAG	GGTAATGGTGCAGGGAAAGAAGATCAAGCTTATTTTGATCCAAGTGCTCCACCACCCTTC**T**AGATTGCAAATATCAGAGCAGCAATTCCAAAACATTGCTGGGAGAAGAACACATTGAGAT	6953
	ATCTCAATGTGTTCTTCTCCCAGCAATGTTTTGGAATTGCTGCTCTGATATTTGCAATCT**A**GAAGGGTGGTGGAGCACTTGGATCAAAATAAGCTTGATCTTCTTTCCCTGCACCATTACC	6954
	CACCCTTC**T**AGATTGCA	6955
	TGCAATCT**A**GAAGGGTG	6956
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Arg36Term AGA-TGA	AAAGAAGATCAAGCTTATTTTGATCCAAGTGCTCCACCACCCTTCAAGATTGCAAATATC**T**GAGCAGCAATTCCAAAACATTGCTGGGAGAAGAACACATTGAGATCTCTGAGTTATGTTC	6957
	GAACATAACTCAGAGATCTCAATGTGTTCTTCTCCCAGCAATGTTTTGGAATTGCTGCTC**A**GATATTTGCAATCTTGAAGGGTGGTGGAGCACTTGGATCAAAATAAGCTTGATCTTCTTT	6958
	CAAATATC**T**GAGCAGCA	6959
	TGCTGCTC**A**GATATTTG	6960
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Leu41Term AAA-TAA	TATTTTGATCCAAGTGCTCCACCACCCTTCAAGATTGCAAATATCAGAGCAGCAATTCCA**T**AACATTGCTGGGAGAAGAACACATTGAGATCTCTGAGTTATGTTCTGAGGGATGTGTTGG	6961
	CCAACACATCCCTCAGAACATAACTCAGAGATCTCAATGTGTTCTTCTCCCAGCAATGTT**A**TGGAATTGCTGCTCTGATATTTGCAATCTTGAAGGGTGGTGGAGCACTTGGATCAAAATA	6962
	CAATTCCA**T**AACATTGC	6963
	GCAATGTT**A**TGGAATTG	6964

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Glu8Term GAG-TAG	CATCCACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGGCTCGTGCTCTCC**T**AGTGCTCGGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGC	6965
	GCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGAGCACT**A**GGAGAGCACGAGCCGGGCCATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGGGTGGATG	6966
	TGCTCTCC**T**AGTGCTCG	6967
	CGAGCACT**A**GGAGAGCA	6968
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Cys9Term TGC-TGA	ACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGGCTCGTGCTCTCCGAGTG**A**TCGGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGCGGTCA	6969
	TGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGA**T**CACTCGGAGAGCACGAGCCGGGCCATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGGGT	6970
	TCCGAGTG**A**TCGGGCCT	6971
	AGGCCCGA**T**CACTCGGA	6972
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Ser10Term TCG-TAG	CCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGGCTCGTGCTCTCCGAGTGCT**A**GGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGCGGTCACC	6973
	GGTGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGGGCGCGAGGCCC**T**AGCACTCGGAGAGCACGAGCCGGGCCATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGG	6974
	CGAGTGCT**A**GGGCCTCG	6975
	CGAGGCCC**T**AGCACTCG	6976
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Ser29Term TCA-TGA	GCTCGGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGCGGT**G**ACCCCCCGCGCTCTCCGCGGCGCCGCGCCGTCGTCCCGCGTCCGCGTCCATCCACCGCGA	6977
	TCGCGGTGGATGGACGCGGACGCGGACGACGGCGCGGCGCCGCGGAGAGCGCGGGGGGT**C**ACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGAGC	6978
	GGCGCGGT**G**ACCCCCCG	6979
	CGGGGGGT**C**ACCGCGCC	6980
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Glu8Term GAG-TAG	CCCCCTCCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCG**T**AGCAGGAGGCGAGCTGCAAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGC	6981
	GCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTTGCAGCTCGCCTCCTGCT**A**CGGCCTCATTGCGGGGGCCATGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGGAGGGGG	6982

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGAGGCCGTAGCAGGAG	6983
	CTCCTGCTACGGCCTCA	6984
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Gln9Term CAG-TAG	CCTCCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGGAGTAGGAGGCGAGCTGCAAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGCCGC	6985
	GCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTTGCAGCTCGCCTCCTACTCCGGCCTCATTGCGGGGGCCATGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGGAGG	6986
	GGCCGGAGTAGGAGGCG	6987
	CGCCTCCTACTCCGGCC	6988
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Glu10Term GAG-TAG	CCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGGAGCAGTAGGCGAGCTGCAAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGCCGCCGC	6989
	GCGGCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTTGCAGCTCGCCTACTGCTCCGGCCTCATTGCGGGGGCCATGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGG	6990
	CGGAGCAGTAGGCGAGC	6991
	GCTCGCCTACTGCTCCG	6992
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Cys13Term TGC-TGA	ACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGGAGCAGGAGGCGAGCTGAAAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGCCGCCGCCCTTCCGCATC	6993
	GATGCGGAAGGGCGGCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTTTCAGCTCGCCTCCTGCTCCGGCCTCATTGCGGGGGCCATGGCCGCGGATGGATCTGTGCGT	6994
	GCGAGCTGAAAGGCCAC	6995
	GTGGCCTTTCAGCTCGC	6996
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Ser4Term TCG-TAG	CTTCACAAATCACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATGGCGGCGTAGGCGACCCAGGAGGCCGACTGCAAGGCTTCCGAGGACGCCCGTCTCTTCTTCGACGCCGC	6997
	GCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGCCTTGCAGTCGGCCTCCTGGGTCGCCTACGCCGCCATTGCCGCCGGGGTGTCGTGGTGGATCTGATTCCGATTTGTGATTTGTGAAG	6998
	GGCGGCGTAGGCGACCC	6999
	GGGTCGCCTACGCCGCC	7000

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Gln7Term CAG-TAG	ATCACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATG GCGGCGTCGGCGACCTAGGAGGCCGACTGCAAGGCTTCCGAGG ACGCCCGTCTCTTCTTCGACGCCGCCAAGCCCC	7001
	GGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGC CTTGCAGTCGGCCTCCTAGGTCGCCGACGCCGCCATTGCCGCCG GGGTGTCGTGGTGGATCTGATTCCGATTTGTGAT	7002
	CGGCGACCTAGGAGGCC	7003
	GGCCTCCTAGGTCGCCG	7004
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Glu8Term GAG-TAG	ACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATGGC GGCGTCGGCGACCCAGTAGGCCGACTGCAAGGCTTCCGAGGACG CCCGTCTCTTCTTCGACGCCGCCAAGCCCCCGC	7005
	GCGGGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGA AGCCTTGCAGTCGGCCTACTGGGTCGCCGACGCCGCCATTGCCG CCGGGGTGTCGTGGTGGATCTGATTCCGATTTGT	7006
	CGACCCAGTAGGCCGAC	7007
	GTCGGCCTACTGGGTCG	7008
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Cys10Term TGC-TGA	TCAGATCCACCACGACACCCCGGCGGCAATGGCGGCGTCGGCGA CCCAGGAGGCCGACTGAAAGGCTTCCGAGGACGCCCGTCTCTTC TTCGACGCCGCCAAGCCCCCGCCCTTCCGCATC	7009
	GATGCGGAAGGGCGGGGGCTTGGCGGCGTCGAAGAAGAGACGG GCGTCCTCGGAAGCCTTTCAGTCGGCCTCCTGGGTCGCCGACGC CGCCATTGCCGCCGGGGTGTCGTGGTGGATCTGA	7010
	GCCGACTGAAAGGCTTC	7011
	GAAGCCTTTCAGTCGGC	7012

WHAT IS CLAIMED IS:

1. An oligonucleotide for targeted alteration of genetic sequence, comprising a single-stranded oligonucleotide having a DNA domain, said DNA domain having at least one mismatch with respect to the genetic sequence to be altered, and further comprising chemical modifications of the oligonucleotide, said chemical modifications selected from the group consisting of an o-methyl modification, an LNA modification including LNA derivatives and analogs, two or more phosphorothioate linkages on a terminus, and a combination of any two or more of these modifications.

2. The oligonucleotide according to claim one that comprises two or more phosphorothioate linkages on at least the 3' terminus.

3. The oligonucleotide according to claim one that comprises a 2'-O-methyl analog.

4. The oligonucleotide according to claim one that comprises an LNA nucleotide, including an LNA derivative or analog.

5. The oligonucleotide according to claim one that comprises a combination of at least two modifications selected from the group of a phosphorothioate linkage, a 2'-O-methyl analog, a locked nucleotide analog and a ribonucleotide.

6. The oligonucleotide according to any one of claims 1 to 5 that comprises at least one unmodified ribonucleotide.

7. The oligonucleotide according to any one of claims 1 to 6, wherein the sequence of said oligonucleotide is selected from the group consisting of SEQ ID NOS: 4341-7012.

8. A method of targeted alteration of genetic material, comprising combining the target genetic material with an oligonucleotide according to any one of claims 1 to 7 in the presence of purified proteins.

9. A method of targeted alteration of genetic material, comprising administering to a cell extract an oligonucleotide of any one of claims 1 to 7.

10. A method of targeted alteration of genetic material, comprising administering to a cell an oligonucleotide of any one of claims 1 to 7.

11. A method of targeted alteration of genetic sequence in callus, comprising administering to the callus an oligonucleotide of any one of claims 1 to 7.

12. A method of targeted alteration of genetic sequence, comprising combining target genetic material with an oligonucleotide according to any one of claims 1 to 7, said target genetic material being a non-transcribed DNA strand of a duplex DNA.

13. The genetic material obtained by any one of the methods of claim 8, 9 or claim 10.

14. A cell comprising the genetic material of claim 13.

15. A plant organism comprising the cell according to claim 14.

16. A plant or plant part produced by the method of claim 11.

17. A method of determining whether an oligonucleotide is optimized for targeted alteration of a genetic sequence, which comprises:

(a) comparing the efficiency of alteration of a targeted genetic sequence by an oligonucleotide of any one of claims 1 to 7 with the efficiency of alteration of the same targeted genetic sequence by a second oligonucleotide, said second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2'-O-methylated oligonucleotide and a chimeric double-stranded double hairpin containing RNA and DNA nucleotides.

18. The method of claim 17 in which the alteration is produced in a plant cell extract.

19. The method of claim 17 in which the alteration is produced in a cell.

20. A kit comprising the oligonucleotide according to any one of claims 1 to 7 and a second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2-O-methylated oligonucleotide and a chimeric double stranded double hairpin containing RNA and DNA nucleotides.

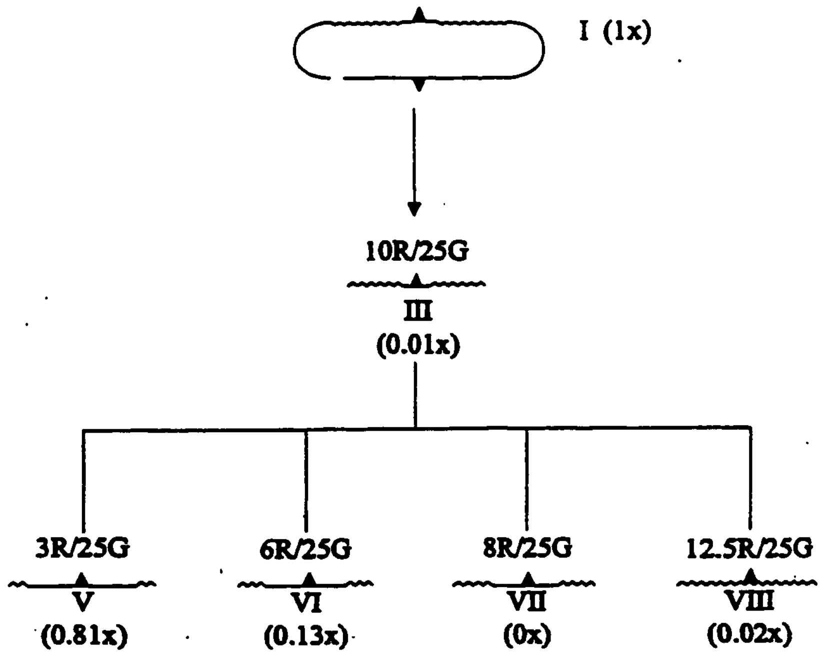


Figure 1A

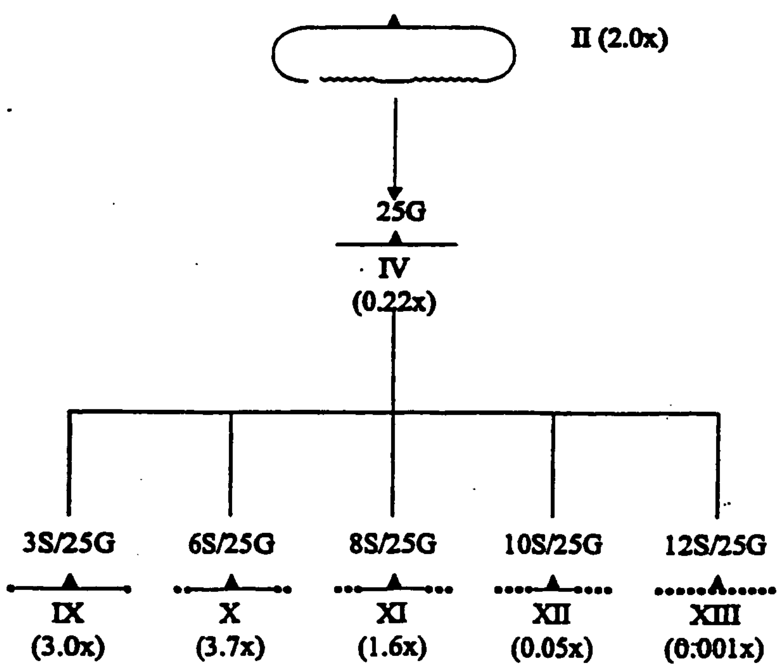


Figure 1B

Plasmids, DNA targets and chimeric oligonucleotides

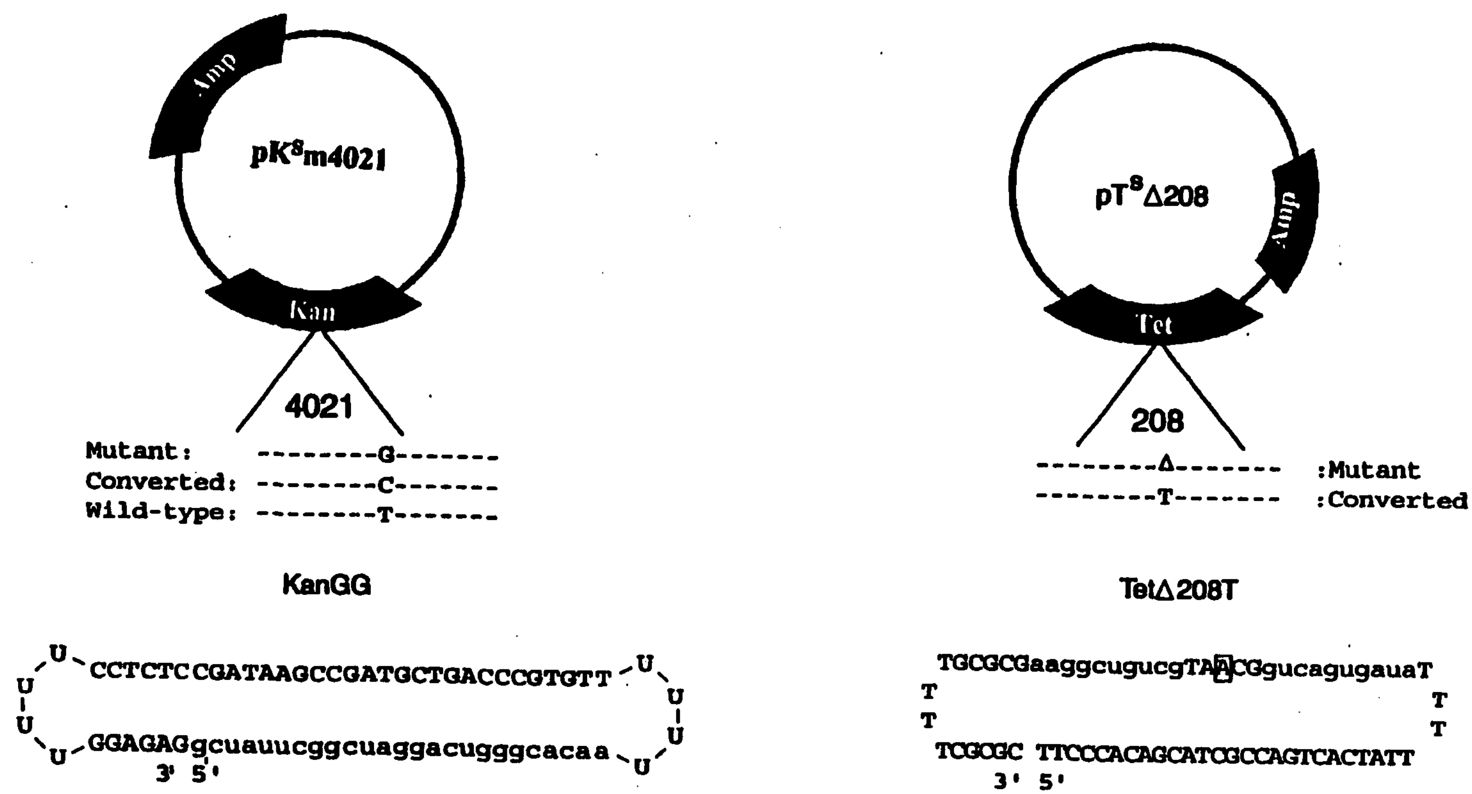


Figure 1C

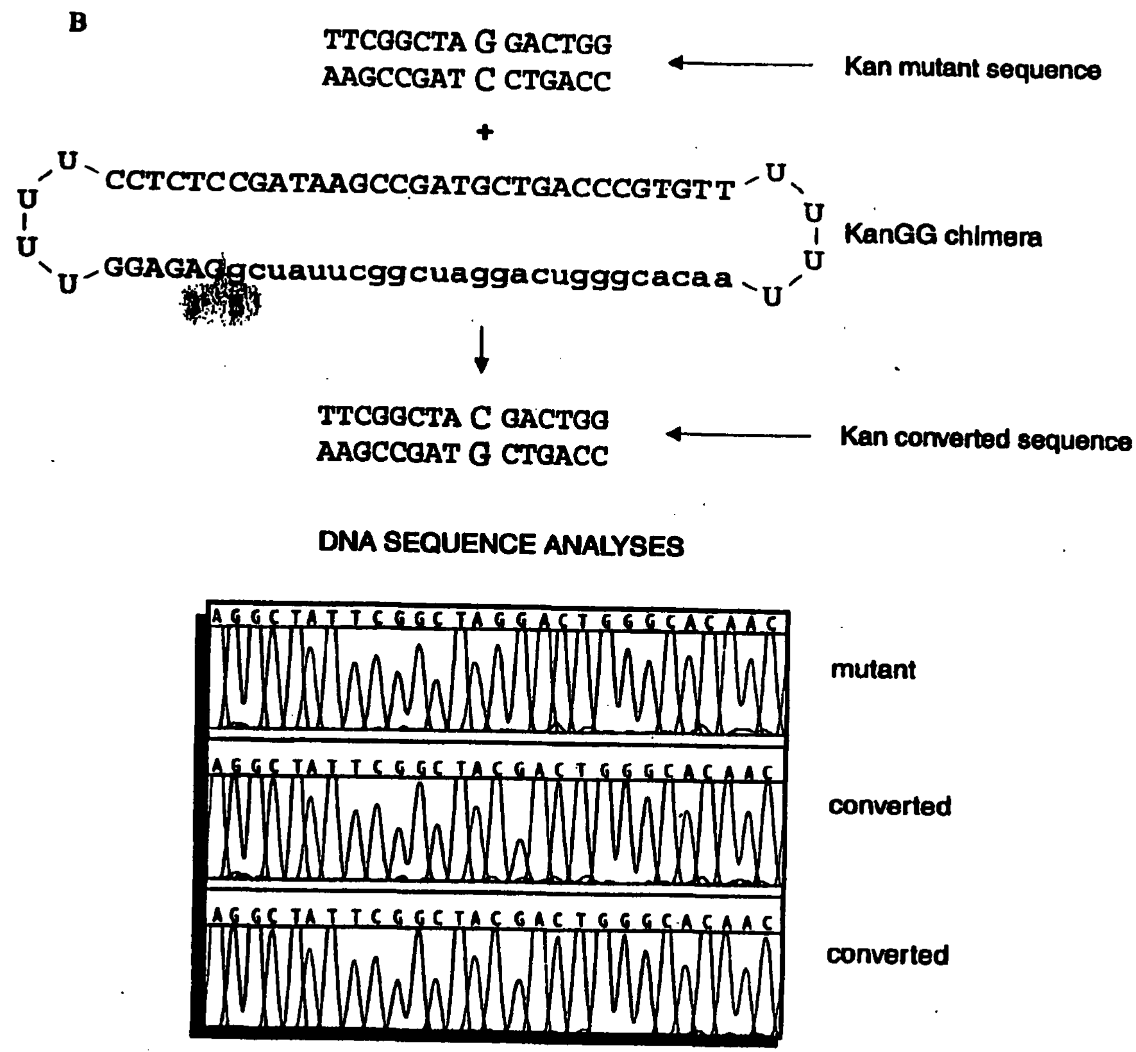

B
TTCGGCTA G GACTGG
AAGCCGAT C CTGACC
Kan mutant sequence
+
CCTCTCCGATAAGCCGATGCTGACCCGTGTT
GGAGAGgcuauucggcuaggacugggcacaa
KanGG chimera
TTCGGCTA C GACTGG
AAGCCGAT G CTGACC
Kan converted sequence
DNA SEQUENCE ANALYSES
AGGCTATTCGGCTAGGACTGGGCACAAC
mutant
AGGCTATTCGGCTACGACTGGGCACAAC
converted
AGGCTATTCGGCTACGACTGGGCACAAC
converted

Figure 1D

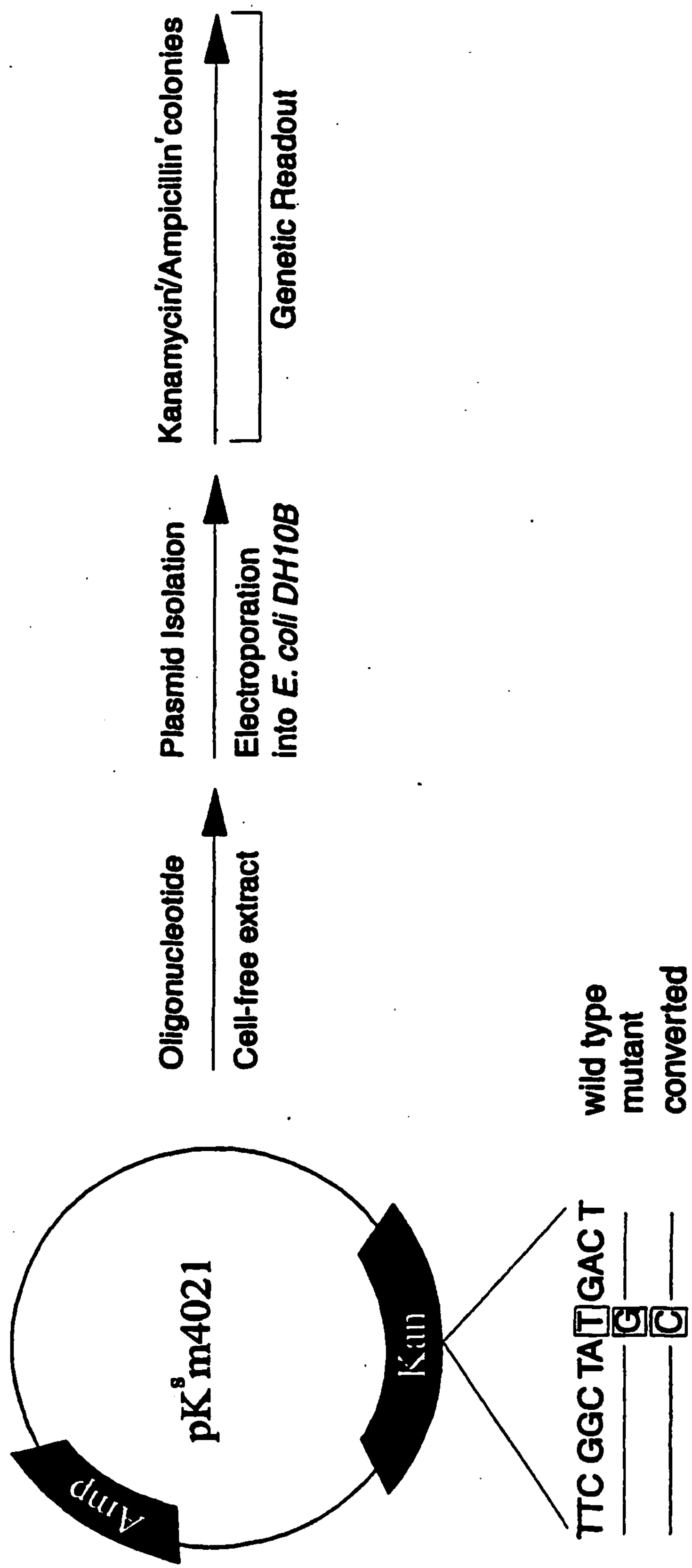
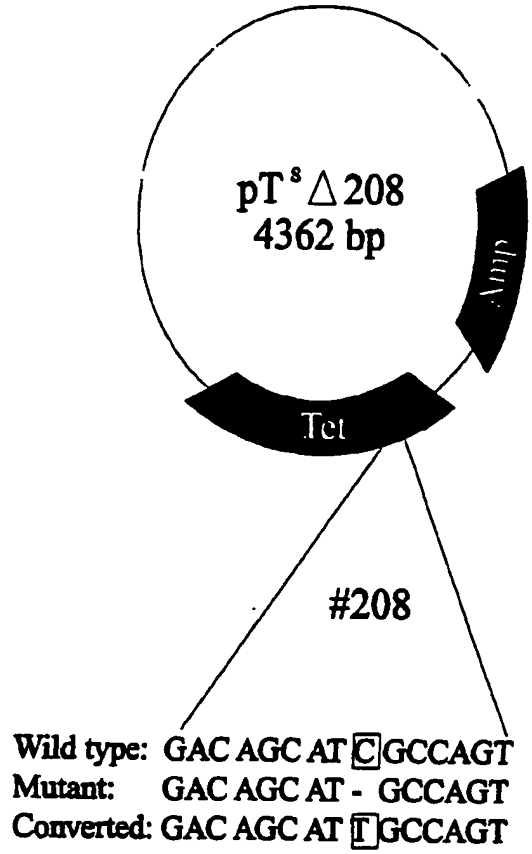

Oligonucleotide
Cell-free extract
Plasmid Isolation
Electroporation
into E. coli DH10B
Kanamycin'/Ampicillin' colonies
Genetic Readout
pK^{s}m4021
Amp
Kan
TTC GGC TA T GAC T
G
C
wild type
mutant
converted

Figure 2



Sequence analysis of Tet[r] plasmid △208

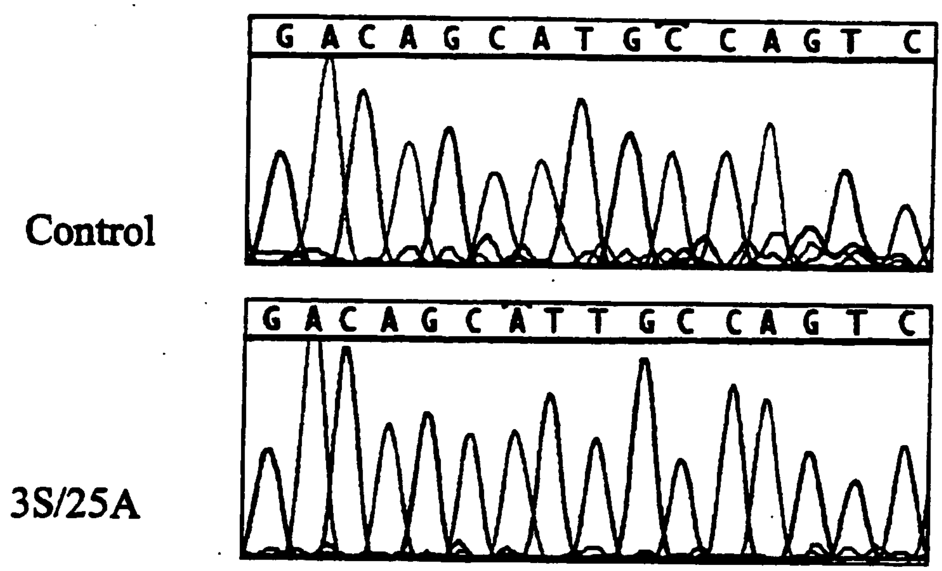


Figure 3

DNA sequence analysis of Kan^r plasmids

Target codon distribution

oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)	—	+	—	—	—
2) 6S/25G (20)	—	+	—	—	—
3) 8S/25G (20)	—	+	—	—	—
4) 10S/25G (18)	—	+	—	+(2)	+(2)
5) 25S/25G (4)	—	—	+(2)	+(2)	—

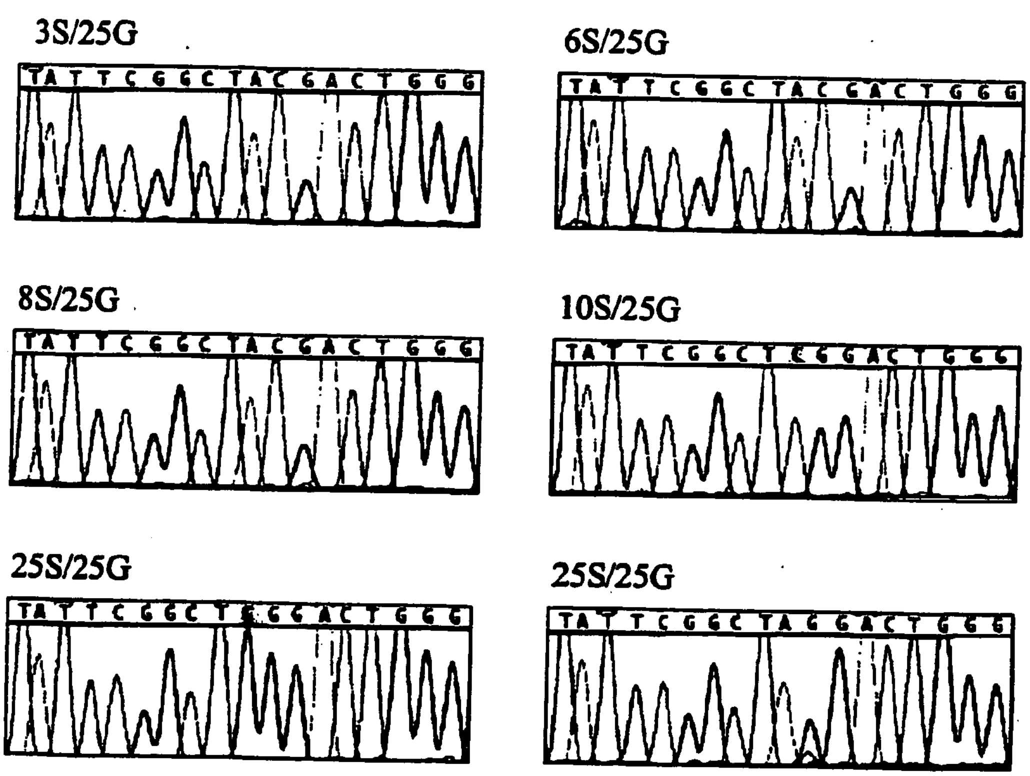


Figure 4

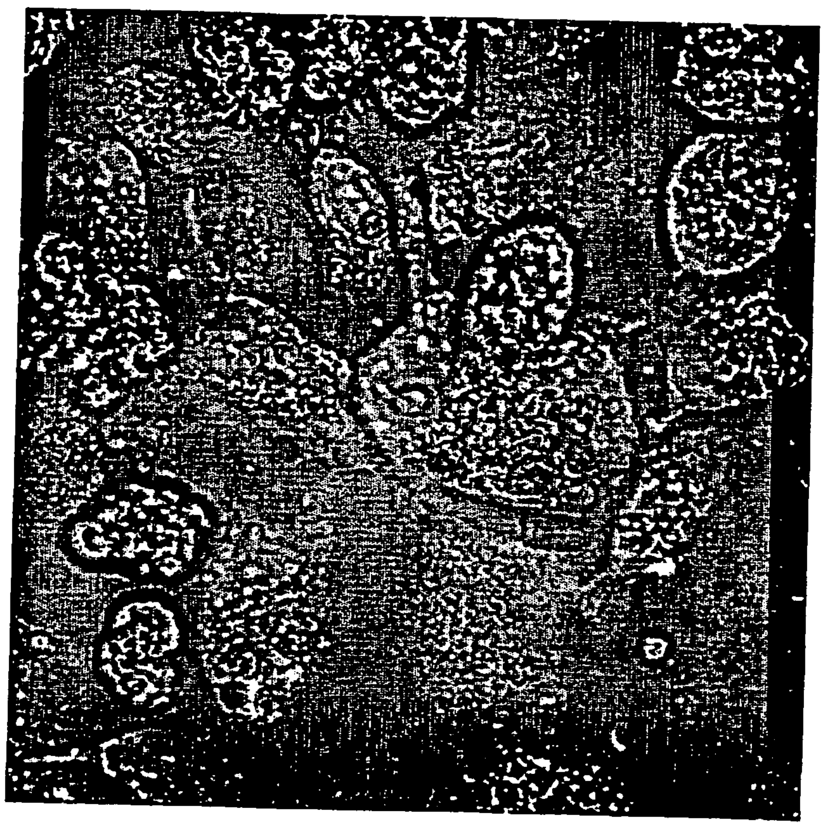


Figure 5

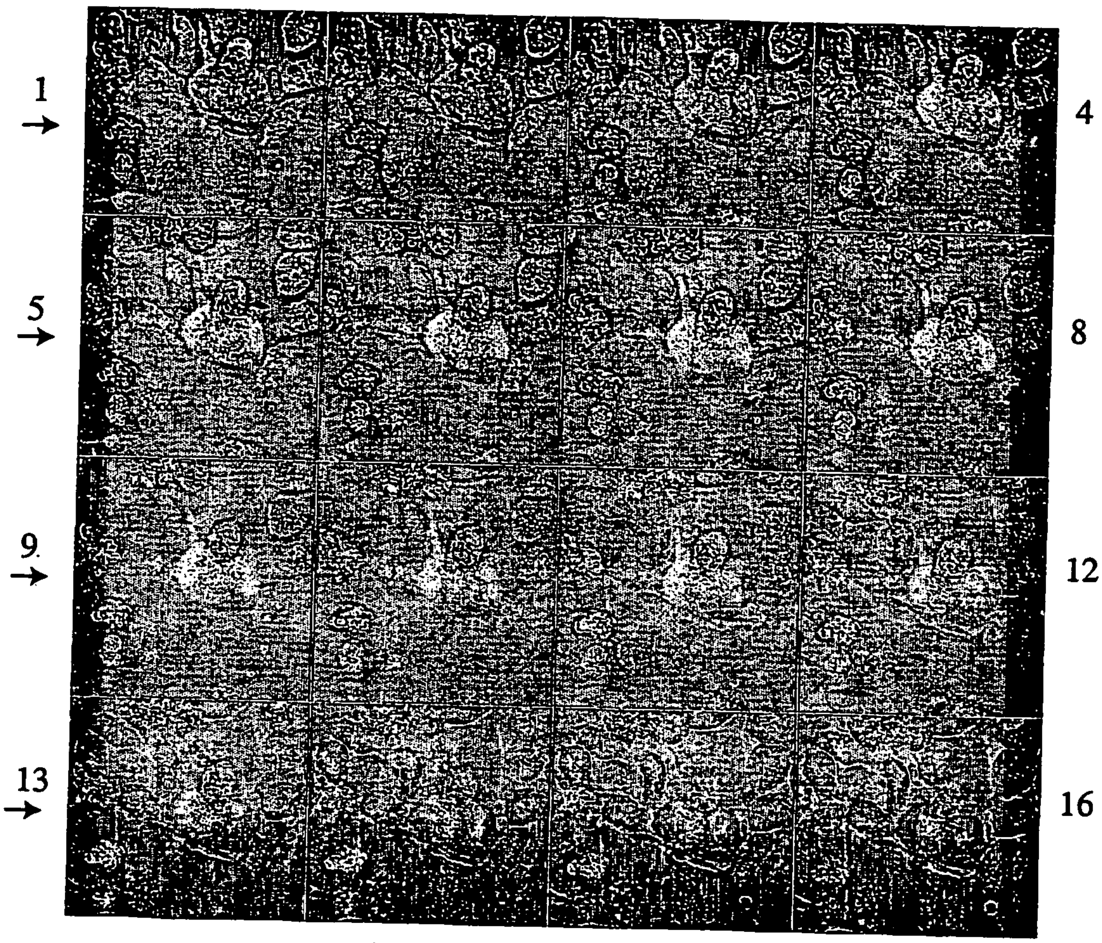


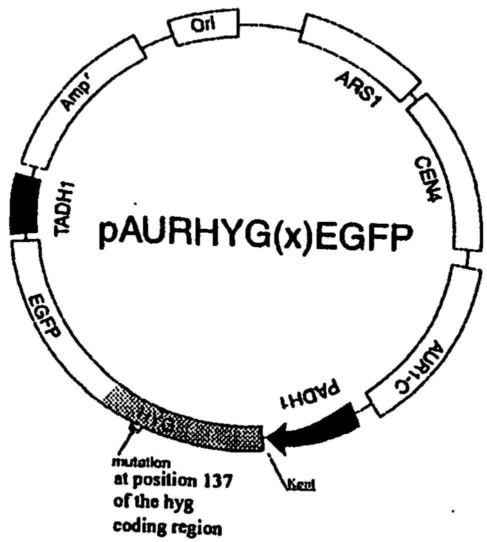
Figure 6

Sequence of normal allele:	GTGGATATGTCCT
Target/existing mutant:	GTGGATAATGTCCT
Desired alteration:	GTGGATACGTCCT

Figure 7A

Sequence of normal allele:	GTGGATATGTCCT
Target/existing mutant:	GTGGATAGGTCCT
Desired alteration:	GTGGATACGTCCT

Figure 7B



HygE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

HygE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG CCG ATG GTT TCT AC-3'

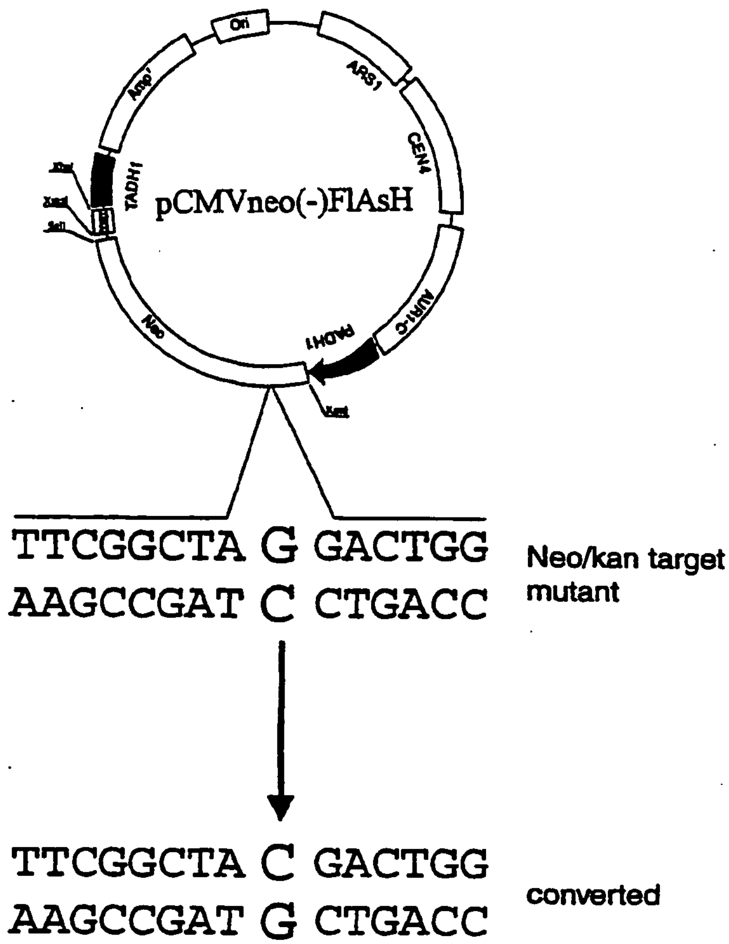
HygE3T/74α: 5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA GCT GAA AGC ACG AG-3'

HygGG/Rev:

```
  T                                          T
 / \                                        / \
T   ACATCCTCCCGCACCTATGCAGGACGCCCAT   T
T   TGTAGGagggcguggaTAGGTccugcggua   T
 \ /       / \                          \ /
  T     3'    5'                          T
```

Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG A-3'

Figure 8



FUSION GENE FOR LIGAND BINDING

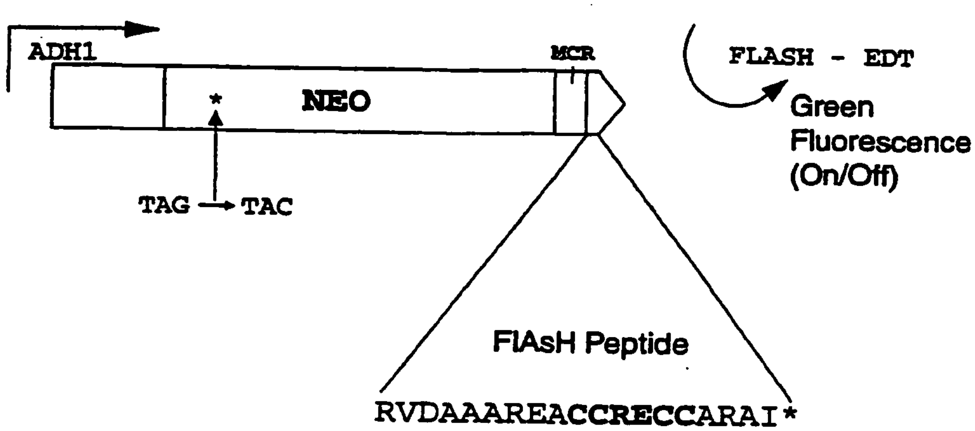


Figure 9

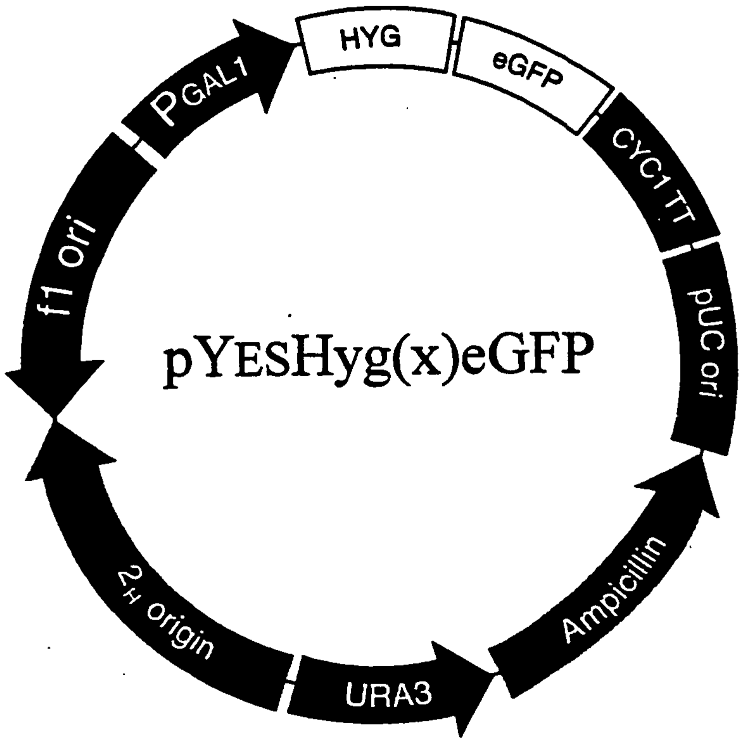

HYG
eGFP
CYC1 TT
pUC ori
Ampicillin
URA3
2μ origin
f1 ori
PGAL1
pYESHyg(x)eGFP

Figure 10

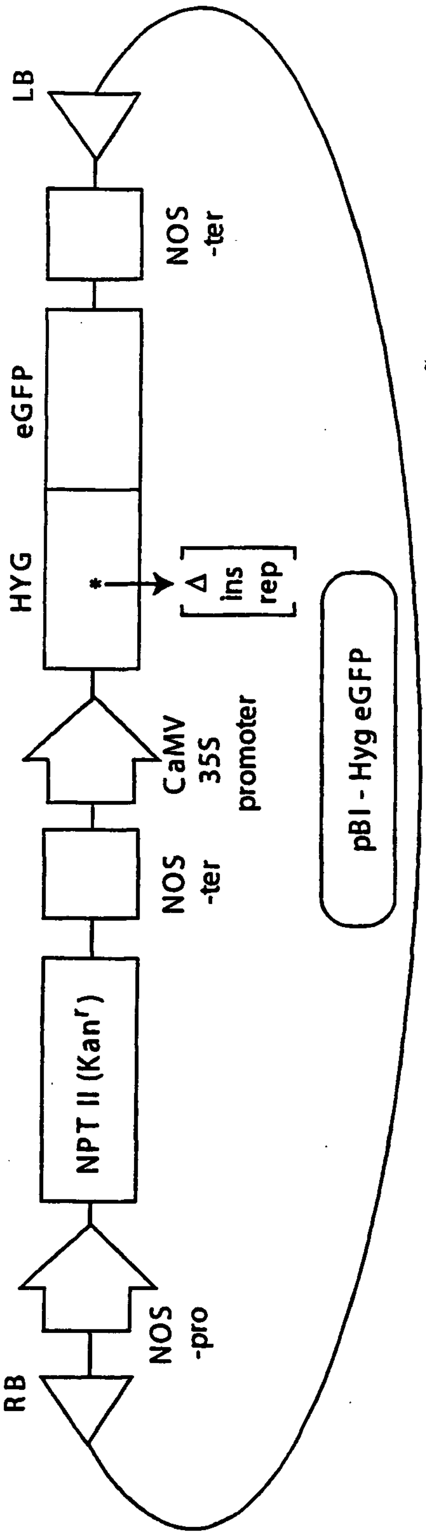

LB
NOS
-ter
eGFP
HYG
*
Δ
ins
rep
CaMV
35S
promoter
NOS
-ter
NPT II (Kan[r])
NOS
-pro
RB
pBI - Hyg eGFP

Figure 11